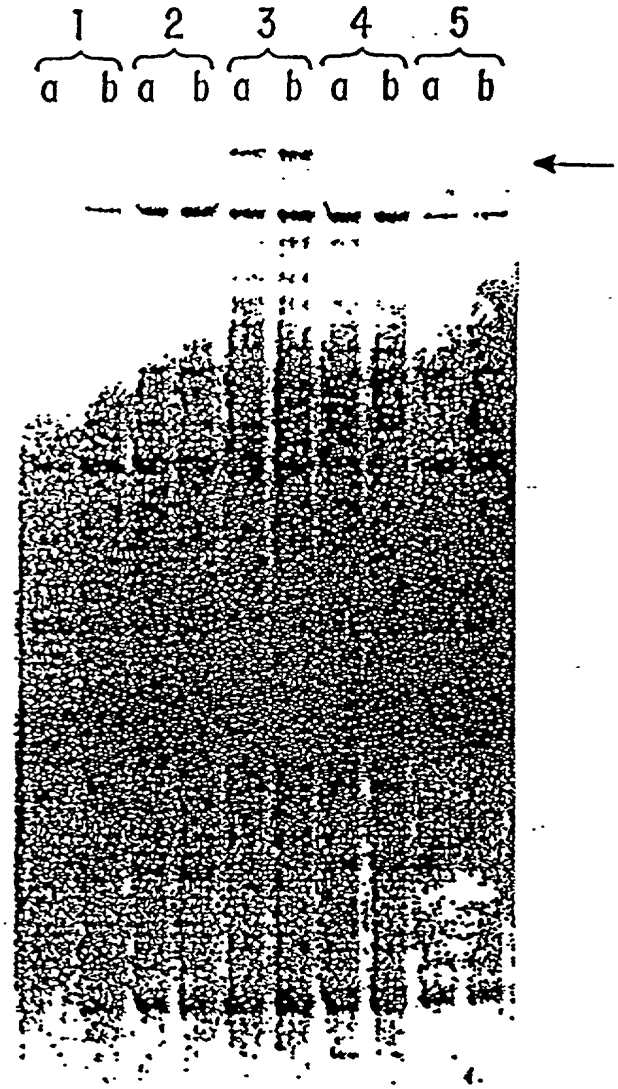

FIG. 1

```
        10         20         30         40         50         60
CTGGTGAGGG GGATCTACAA CTTGTTCGGT TAAAGAAAAA AGCAACAGCC AACAGAAATG  60
TGGTTATCCT TCACCTACCT AAAAAGGGAG ATGATGTGAA ACCAGGAACC AGATGCCGAG 120
TAGCAGGATG GGGGAGATTT GGCAATAAGT CAGCTCCCTC TGAAACTCTG AGAGAAGTCA 180
ACATCACTGT CATAGACAGA AAAATCTGCA ATGATGAAAA ACACTATAAT TTTCATCCTG 240
TAATTGGTCT AAACATGATT TGGGCAGGGG ACCTCCCCGG CGGAAAGGAC TCCTGCAATG 300
GGGATTCTGG CAGCCCTCTC CTATGTGATT GGTATTTGGG AAGCATCACC TCCTTTT    357
```

FIG. 2

```
        10         20         30         40         50         60
TTAGCGCCAT TGCCATAGAG AGACCTCAGC CATCAATCAC TAGCACATGA TTGACAGACA  60
GAGAATGGGA CTTTGGGCTT TGGCAATTCT GACACTTCCC ATGTATTTGA CAGTTACGGA 120
GGGCAGTAAA TCGTCCTGGG GTCTGGAAAA TGAGGCTTTA ATTGTGAGAT GCCCCCAAAG 180
AGGACGCTCG ACTTATCCTG TGGAATGGTA TTACTCAGAT ACAAATGAAA GTATTCCTAC 240
CCAAAAAAAA AAAAA
                                                                  255
```

FIG. 4A

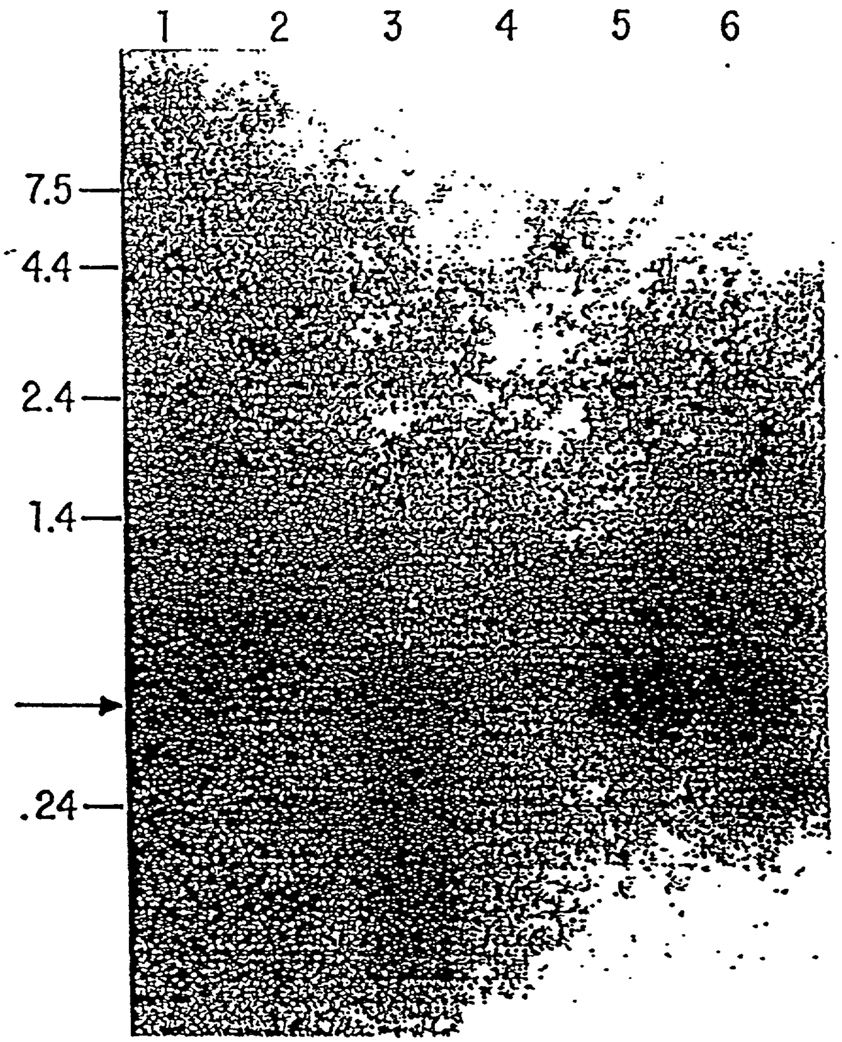

FIG. 3

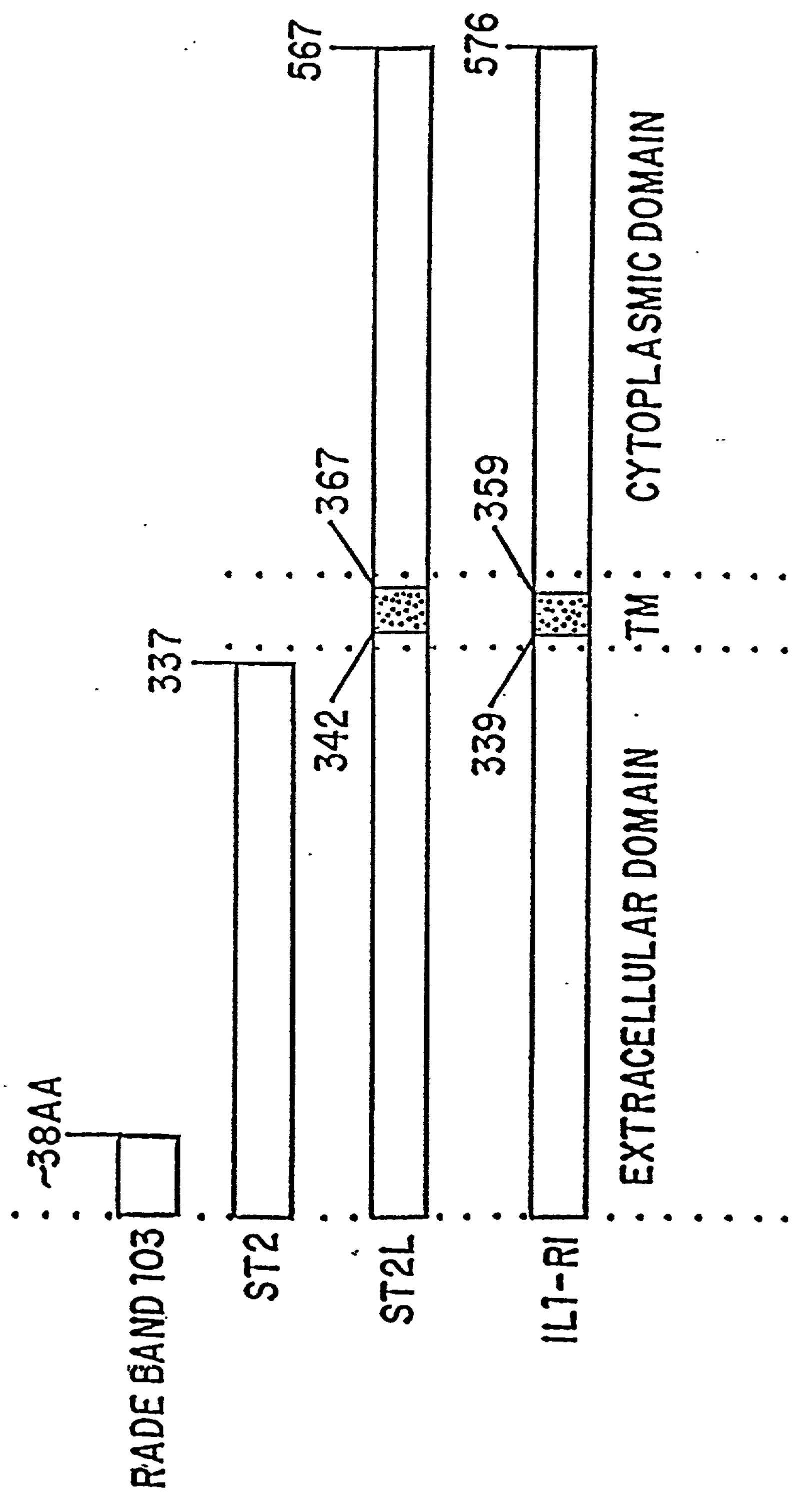
~38AA
RADE BAND 103
ST2
337
ST2L
342
367
567
IL1-RI
339
359
576
EXTRACELLULAR DOMAIN
TM
CYTOPLASMIC DOMAIN

FIG. 4B

1 atgattgaca gacagagaat gggactttgg gctttggcaa ttctgacact tcccatgtat
61 ttgacagtta cggagggcag taaatcgtcc tggggtctgg aaaatgaggc tttaattgtg
121 agatgccccc aaagaggacg ctcgacttat cctgtggaat ggtattactc agatacaaat
181 gaaagtattc ctactcaaaa aagaaatcgg atctttgtct caagagatcg tctgaagttt
241 ctaccagcca gagtcgaaga ctctgggatt tatgcttgtg ttatcagaag ccccaacttg
301 aataagactg gatacttgaa tgtcaccata cataaaaagc cgccaagctg caatatccct
361 gattatttga tgtactcgac agtacgtgga tcagataaaa atttcaagat aagctgtcca
421 acaattgacc tgtataattg gacagcacct gttcagtggt ttaagaactg caaagctctc
481 caagagccaa ggttcagggc acacaggtcc tacttgttca ttgacaacgt gactcatgat
541 gatgaaggtg actacacttg tcaattcaca cacgcggaga atggaaccaa ctacatcgtg
601 acggccacca gatcattcac agttgaagaa aaaggctttt ctatgtttcc agtaattaca
661 aatcctccat acaaccacac aatggaagtg gaaataggaa aaccagcaag tattgcctgt
721 tcagcttgct ttggcaaagg ctctcacttc ttggctgatg tcctgtggca gattaacaaa
781 acagtagttg gaaattttgg tgaagcaaga attcaagaag aggaaggtcg aaatgaaagt
841 tccagcaatg acatggattg tttaacctca gtgttaagga taactggtgt gacagaaaag
901 gacctgtccc tggaatatga ctgtctggcc ctgaaccttc atggcatgat aaggcacacc
961 ataaggctga gaaggaaaca accaagtaag gagtgtccct cacacattgc t

FIG. 4C

MIDRQRMGLWALAILTLPMYLTVTEGSKSSWGLENEALIVRCPQRGRSTYPVEWYYSD
TNESIPTQKRNRIFVSRDRLKFLPARVEDSGIYACVIRSPNLNKTGYLNVTIHKKPPSCNIP
DYLMYSTVRGSDKNFKITCPTIDLYNWTAPVQWFKNCKALQEPRFRAHRSYLFIDNVTH
DDEGDYTCQFTHAENGTNYIVTATRSFTVEEKGFSMFPVITNPPYNHTMEVEIGKPASIA
CSACFGKGSHFLADVLWQINKTVVGNFGEARIQEEEGRNESSSNDMDCLTSVLRITGVT
EKDLSLEYDCLALNLHGMIRHTIRLRRKQPSKECPSHIA

FIG. 4D

```
ATGATTGACA GACAGAGAAT GGGACTTTGG GCTTTGGCAA TTCTGACACT TCCCATGTAT    60
TTGACAGTTA CGGAGGGCAG TAAATCGTCC TGGGGTCTGG AAAATGAGGC TTTAATTGTG   120
AGATGCCCCC AAAGAGGACG CTCGACTTAT CCTGTGGAAT GGTATTACTC AGATACAAAT   180
GAAAGTATTC CTACTCAAAA AAGAAATCGG ATCTTTGTCT CAAGAGATCG TCTGAAGTTT   240
CTACCAGCCA GAGTGGAAGA CTCTGGGATT TATGCTTGTG TTATCAGAAG CCCCAACTTG   300
AATAAGACTG GATACTTGAA TGTCACCATA CATAAAAAGC CGCCAAGCTG CAATATCCCT   360
GATTATTTGA TGTACTCGAC AGTACGTGGA TCAGATAAAA ATTTCAAGAT AACGTGTCCA   420
ACAATTGACC TGTATAATTG GACAGCACCT GTTCAGTGGT TTAAGAACTG CAAAGCTCTC   480
CAAGAGCCAA GGTTCAGGGC ACACAGGTCC TACTTGTTCA TTGACAACGT GACTCATGAT   540
GATGAAGGTG ACTACACTTG TCAATTCACA CACGCGGAGA ATGGAACCAA CTACATCGTG   600
ACGGCCACCA GATCATTCAC AGTTGAAGAA AAAGGCTTTT CTATGTTTCC AGTAATTACA   660
AATCCTCCAT ACAACCACAC AATGGAAGTG GAAATAGGAA AACCAGCAAG TATTGCCTGT   720
TCAGCTTGCT TTGGCAAAGG CTCTCACTTC TTGGCTGATG TCCTGTGGCA GATTAACAAA   780
ACAGTAGTTG GAAATTTTGG TGAAGCAAGA ATTCAAGAAG AGGAAGGTCG AAATGAAAGT   840
TCCAGCAATG ACATGGATTG TTTAACCTCA GTGTTAAGGA TAACTGGTGT GACAGAAAAG   900
GACCTGTCCC TGGAATATGA CTGTCTGGCC CTGAACCTTC ATGGCATGAT AAGGCACACC   960
ATAAGGCTGA GAAGGAAACA ACCAATTGAT CACCGAAGCA TCTACTACAT AGTTGCTGGA  1020
TGTAGTTTAT TGCTAATGTT TATCAATGTC TTGGTGATAG TCTTAAAAGT GTTCTGGATT  1080
GAGGTTGCTC TGTTCTGGAG AGATATAGTG ACACCTTACA AAACCCGGAA CGATGGCAAG  1140
CTCTACGATG CGTACATCAT TTACCCTCGG GTCTTCCGGG GCAGCGCGGC GGGAACCCAC  1200
TCTGTGGAGT ACTTTGTTCA CCACACTCTG CCCGACGTTC TTGAAAATAA ATGTGGCTAC  1260
AAATTGTGCA TTTATGGGAG AGACCTGTTA CCTGGGCAAG ATGCAGCCAC CGTGGTGGAA  1320
AGCAGTATCC AGAATAGCAG AAGACAGGTG TTTGTTCTGG CCCCTCACAT GATGCACAGC  1380
AAGGAATTTG CCTACGAGCA GGAGATTGCT CTGCACAGCG CCCTCATCCA GAACAACTCC  1440
AAGGTGATTC TTATTGAAAT GGAGCCTCTG GGTGAGGCAA GCCGACTACA GGTTGGGGAC  1500
CTGCAAGATT CTCTCCAGCA TCTTGTGAAA ATTCAGGGGA CCATCAAGTG GAGGGAAGAT  1560
CATGTGGCCG ACAAGCAGTC TCTAAGTTCC AAATTCTGGA AGCATGTGAG GTACCAAATG  1620
CCAGTGCCAG AAAGAGCCTC CAAGACGGCA TCTGTTGCGG CTCCGTTGAG TGGCAAGGCA  1680
TGCTTAGACC TGAAACACTT TTGA                                         1704
```

FIG. 4E

MIDRQRMGLWALAILTLPMYLTVTEGSKSSWGLENEALIVRCPQRGRSTYPVEWYYSD
TNESIPTQKRNRIFVSRDRLKFLPARVEDSGIYACVIRSPNLNKTGYLNVTIHKKPPSCNIP
DYLMYSTVRGSDKNFKITCPTIDLYNWTAPVQWFKNCKALQEPRFRAHRSYLFIDNVTH
DDEGDYTCQFTHAENGTNYIVTATRSFTVEEKGFSMFPVITNPPYNHTMEVEIGKPASIA
CSACFGKGSHFLADVLWQINKTVVGNFGEARIQEEEGRNESSSNDMDCLTSVLRITGVT
EKDLSLEYDCLALNLHGMIRHTIRLRRKQPIDHRSIYYIVAGCSLLLMFINVLVIVLKVFW
IEVALFWRDIVTPYKTRNDGKLYDAYIIYPRVFRGSAAGTHSVEYFVHHTLPDVLENKC
GYKLCIYGRDLLPGQDAATVVESSIQNSRRQVFVLAPHMMHSKEFAYEQEIALHSALIQ
NNSKVILIEMEPLGEASRLQVGDLQDSLQHLVKIQGTIKWREDHVADKQSLSSKFWKHV
RYQMPVPERASKTASVAAPLSGKACLDLKHF

FIG. 4F

1 atctcaacaa cgagttacca atacttgctc ttgattgata aacagaatgg ggttttggat
61 cttagcaatt ctcacaattc tcatgtattc cacagcagca aagtttagta aacaatcatg
121 gggcctggaa aatgaggctt taattgtaag atgtcctaga caaggaaaac ctagttacac
181 cgtggattgg tattactcac aaacaaacaa aagtattccc actcaggaaa gaaatcgtgt
241 gtttgcctca ggccaacttc tgaagtttct accagctgaa gttgctgatt ctggtattta
301 tacctgtatt gtcagaagtc ccacattcaa taggactgga tatgcgaatg tcaccatata
361 taaaaaacaa tcagattgca atgttccaga ttatttgatg tattcaacag tatctggatc
421 agaaaaaaat tccaaaattt attgtcctac cattgacctc tacaactgga cagcacctct
481 tgagtggttt aagaattgtc aggctcttca aggatcaagg tacagggcgc acaagtcatt
541 tttggtcatt gataatgtga tgactgagga cgcaggtgat tacacctgta aatttataca
601 caatgaaaat ggagccaatt atagtgtgac ggcgaccagg tccttcacgg tcaaggatga
661 gcaaggcttt tctctgtttc cagtaatcgg agccccctgca caaaatgaaa taaaggaagt
721 ggaaattgga aaaaacgcaa acctaacttg ctctgcttgt tttggaaaag gcactcagtt
781 cttggctgcc gtcctgtggc agcttaatgg aacaaaaatt acagactttg gtgaaccaag
841 aattcaacaa gaggaagggc aaaatcaaag tttcagcaat gggctggctt gtctagacat
901 ggttttaaga atagctgacg tgaaggaaga ggatttattg ctgcagtacg actgtctggc
961 cctgaatttg catggcttga gaaggcacac cgtaagacta agtaggaaaa atccaagtaa
1021 ggagtgtttc tgagactttg atcacctgaa ctttctctag caagtgtaag cagaatggag
1081 tgtggttcca agagatccat caagacaatg ggaatggcct gtgccataaa atgtgcttct
1141 cttcttcggg atgttgtttg ctgtctgatc tttgtagact gttcctgttt gctgggagct
1201 tctctgctgc ttaaattgtt cgtcctcccc cactccctcc tatcgttggt ttgtctagaa
1261 cactcagctg cttctttggt catccttgtt ttctaacttt atgaactccc tctgtgtcac
1321 tgtatgtgaa aggaaatgca ccaacaaccg aaaactg

FIG. 4G

MGFWILAILTILMYSTAAKFSKQSWGLENEALIVRCPRQGKPSYTVDWYYSQTNKSIPT
QERNRVFASGQLLKFLPAEVADSGIYTCIVRSPTFNRTGYANVTIYKKQSDCNVPDYLM
YSTVSGSEKNSKIYCPTIDLYNWTAPLEWFKNCQALQGSRYRAHKSFLVIDNVMTEDAG
DYTCKFIHNENGANYSVTATRSFTVKDEQGFSLFPVIGAPAQNEIKEVEIGKNANLTCSA
CFGKGTQFLAAVLWQLNGTKITDFGEPRIQQEEGQNQSFSNGLACLDMVLRIADVKEED
LLLQYDCLALNLHGLRRHTVRLSRKNPSKECF

FIG. 4H

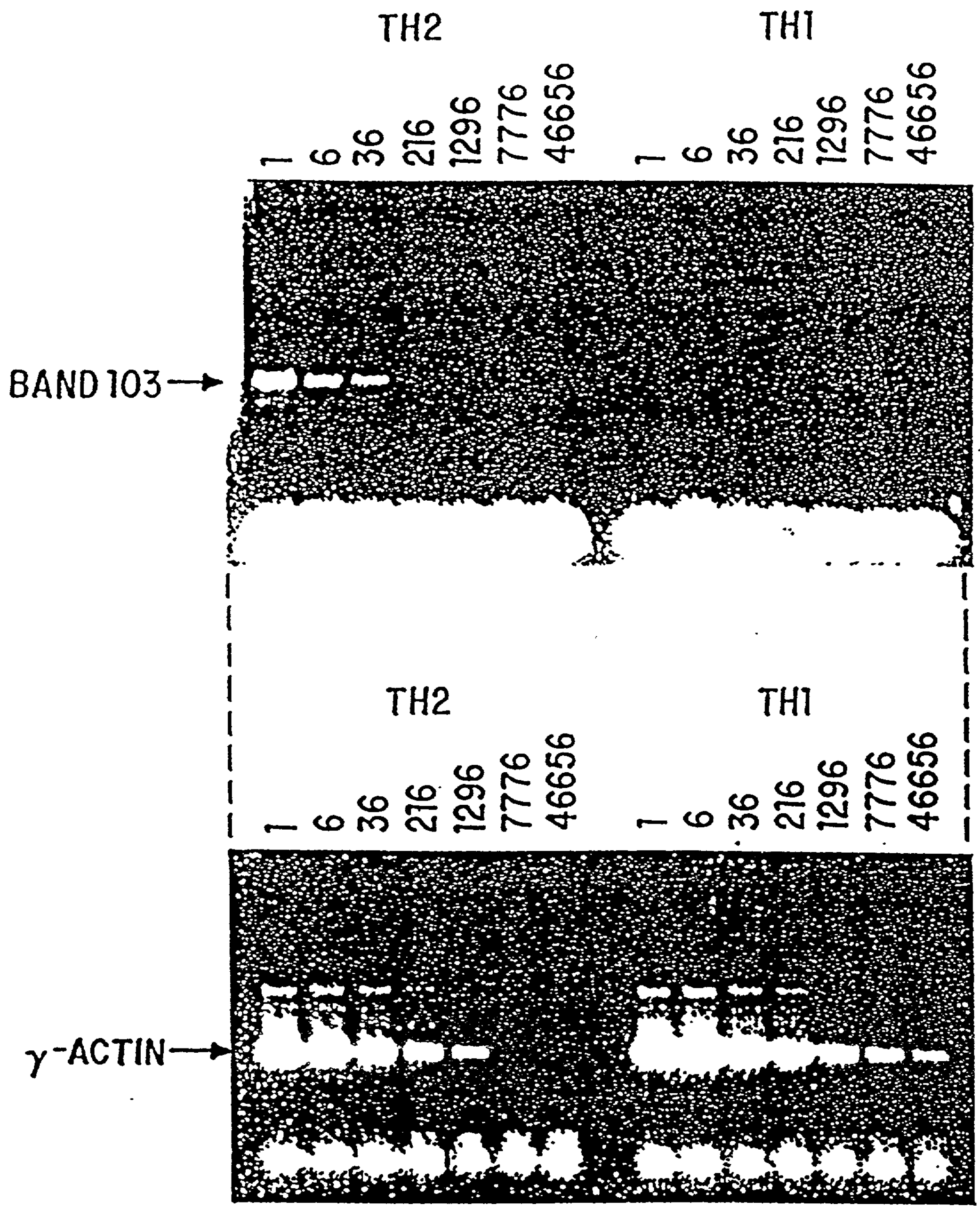
TH2
TH1
1 6 36 216 1296 7776 46656
1 6 36 216 1296 7776 46656
BAND 103
TH2
TH1
1 6 36 216 1296 7776 46656
1 6 36 216 1296 7776 46656
γ-ACTIN

FIG. 5

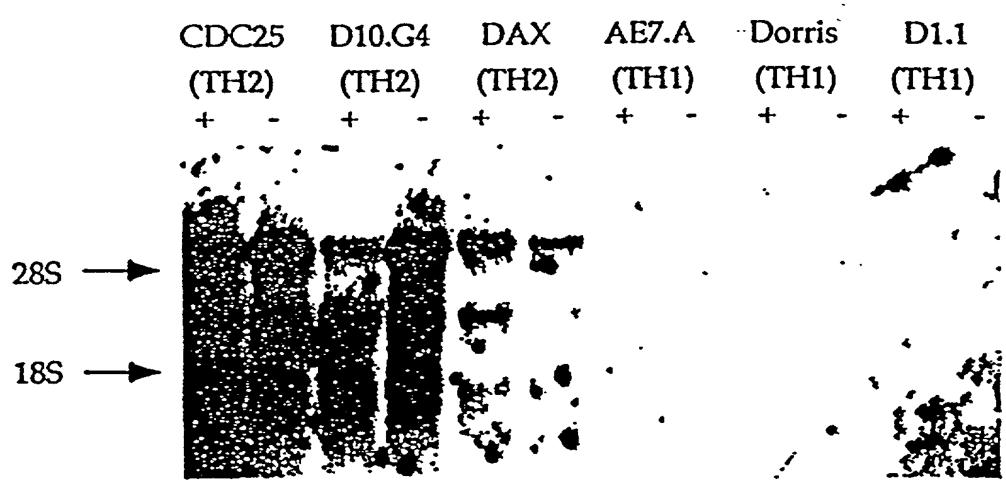
CDC25
(TH2)
D10.G4
(TH2)
DAX
(TH2)
AE7.A
(TH1)
Dorris
(TH1)
D1.1
(TH1)
+ - + - + - + - + - + -
28S
18S

FIG. 6

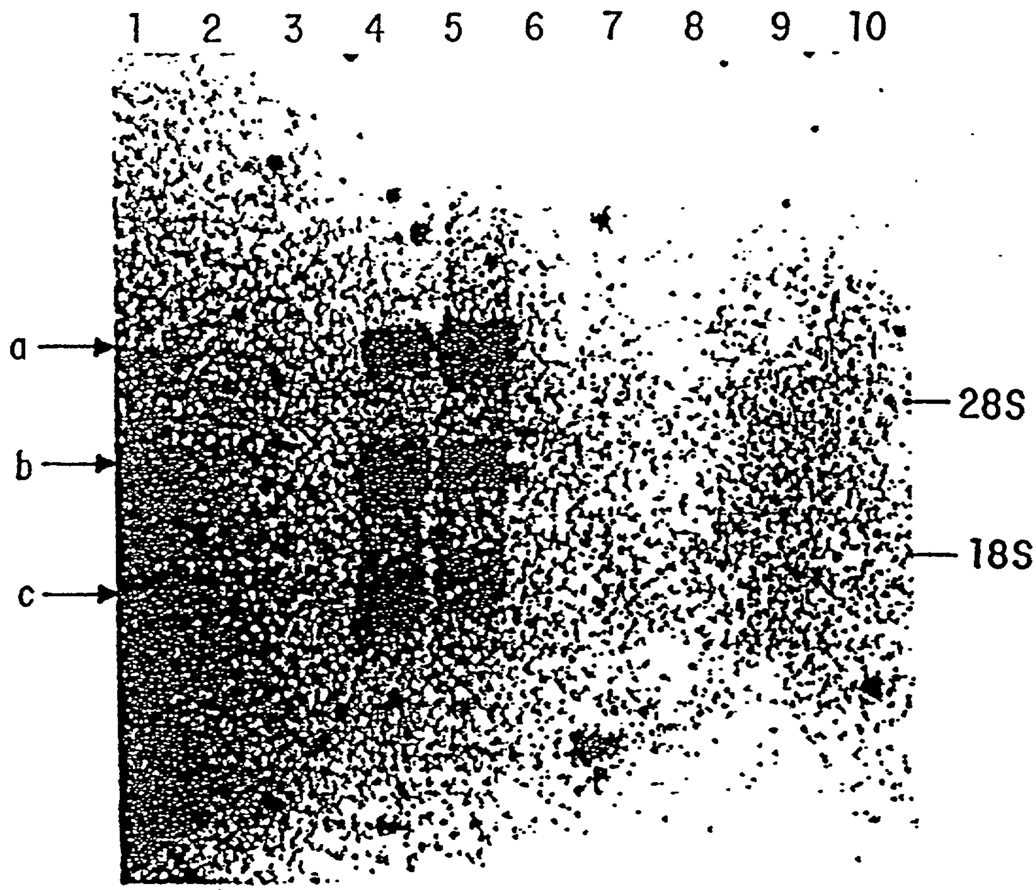

FIG. 7

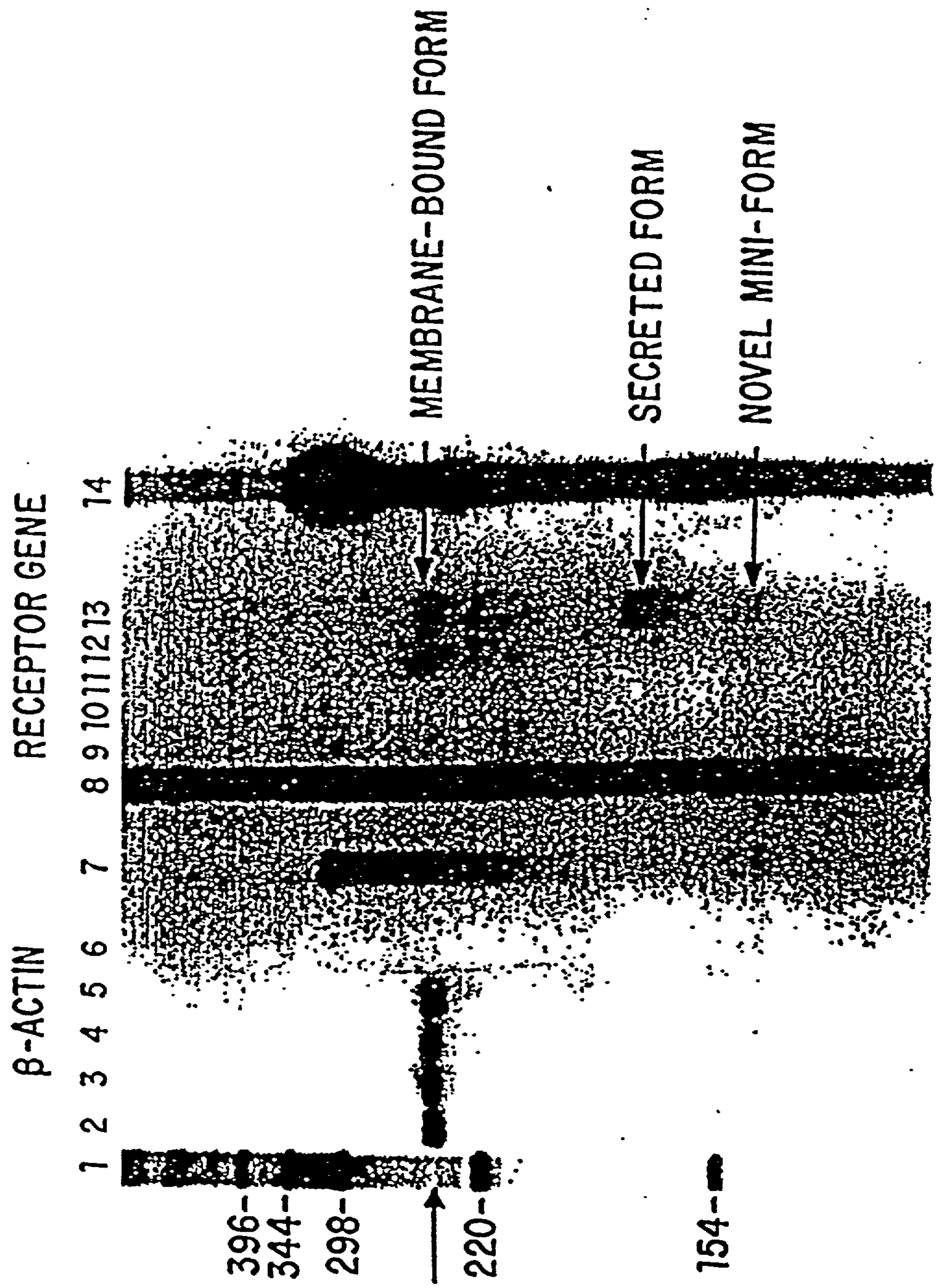
β-ACTIN
RECEPTOR GENE
1 2 3 4 5 6 7 8 9 10 11 12 13 14
MEMBRANE-BOUND FORM
SECRETED FORM
NOVEL MINI-FORM
396-
344-
298-
220-
154-

FIG. 8

```
                                                                        CC   2
GGGTCGACCCACGCGTCCGAGCCTCCTCAGTCAAGAGAAGCATCCCTCCAGAAACAGGGAAACATGACACTTTTGAAAG   81
AATGCCAAACGGCGTGAAAATAAAAACAGAGCATTCCCATTTGCACCGACCAATCTCCAATCTCCTGTAAGATTCAAAA  160
GGGCAAGCAAGAGGCGGTGACCGTTCACGAAAGCTAAAATCCCATGCTATTGAACATGAAGACTTCTGATGCTTAAATC  239
TCATTAACTGCTTTAAGTCACTCCCAGGAGCTTGGATCCCAACTTCTAGCAGTAATAGTCTGTGTAAAAAAAAAAAAAA  318
AATCAGTCTACAACCACTCTCTAAATGCATGGATGAACTCATCAGAACATCAAAACCCAAGGAAACCCTAAGAGAGAAG  397
AATTCTAATAAAAAGAATTTTACATTGAAAACTTACAAGGCAAGGTCCCTTTCCCTGCTGACAGCCTAAGAAGTGATGT  476

                     M   A   M   N   S   M   C   I   E   E   Q   R   H   L   E    15
AACTGCCACTGTGAAGACC ATG GCG ATG AAC AGC ATG TGC ATT GAA GAG CAG CGC CAC CTC GAA  540

 H   Y   L   F   P   V   V   Y   I   I   V   F   I   V   S   V   P   A   N   I    35
CAC TAT TTG TTC CCG GTG GTC TAC ATA ATT GTG TTT ATA GTC AGC GTC CCA GCC AAC ATC  600

 G   S   L   C   V   S   F   L   Q   A   K   K   E   N   E   L   G   I   Y   L    55
GGA TCT TTA TGC GTA TCC TTT CTG CAA GCG AAG AAG GAA AAT GAG CTA GGG ATT TAC CTC  660

 F   S   L   S   L   S   D   L   L   Y   A   L   T   L   P   L   W   I   N   Y    75
TTC AGT CTG TCC CTG TCA GAC CTG CTG TAT GCG CTG ACT CTG CCC CTC TGG ATC AAT TAC  720
```

FIG. 9A

T W N K D N W T F S P T L C K G S V F F 95
ACT TGG AAT AAA GAC AAC TGG ACT TTC TCT CCC ACC TTG TGC AAA GGA AGC GTT TTC TTC 780

T Y M N F Y S S T A F L T C I A L D R Y 115
ACC TAC ATG AAC TTT TAC AGC AGC ACG GCG TTC CTC ACT TGC ATT GCC CTG GAC CGC TAT 840

L A V V Y P L K F S F L R T R R F A F I 135
TTA GCA GTC GTC TAC CCT CTG AAG TTT TCC TTC CTA AGA ACG AGA AGA TTC GCG TTT ATT 900

T S L S I W I L E S F F N S M L L W K D 155
ACC AGC CTC TCC ATC TGG ATA TTA GAG TCC TTC TTT AAC TCT ATG CTT CTG TGG AAA GAT 960

E T S V E Y C D S D K S N F T L C Y D K 175
GAA ACG AGT GTT GAA TAT TGT GAC TCG GAC AAA TCT AAT TTC ACT CTC TGC TAT GAC AAA 1020

Y P L E K W Q I N L N L F R T C M G Y A 195
TAC CCT CTG GAG AAA TGG CAG ATA AAC CTC AAC CTG TTT CGG ACG TGC ATG GGC TAC GCA 1080

I P L I T I M I C N H K V Y R A V R H N 215
ATA CCC TTG ATC ACC ATC ATG ATC TGC AAC CAT AAA GTC TAC CGA GCT GTG CGG CAC AAC 1140

Q A T E N S E K R R I I K L L A S I T L 235
CAA GCC ACG GAA AAC AGC GAG AAG AGA AGG ATC ATA AAG TTG CTT GCT AGC ATC ACG TTG 1200

T F V L C F T P F H V M V L I R C V L E 255
ACT TTC GTC CTA TGC TTT ACC CCC TTC CAC GTG ATG GTG CTC ATC CGC TGC GTT TTA GAG 1260

FIG. 9B

```
 R   D   M   N   V   N   D   K   S   G   W   Q   T   F   T   V   Y   R   V   T   275
CGC GAC ATG AAC GTC AAT GAC AAG TCT GGA TGG CAG ACG TTT ACG GTG TAC AGA GTC ACA 1320

 V   A   L   T   S   L   N   C   V   A   D   P   I   L   Y   C   F   V   T   E   295
GTA GCC CTG ACG AGT CTA AAC TGT GTT GCC GAT CCC ATT CTG TAC TGC TTT GTG ACT GAG 1380

 T   G   R   A   D   M   W   N   I   L   K   L   C   T   R   K   H   N   R   H   315
ACG GGG AGA GCT GAT ATG TGG AAC ATA TTA AAA TTG TGT ACT AGG AAA CAC AAT AGA CAC 1440

 Q   G   K   K   R   D   I   L   S   V   S   T   R   D   A   V   E   L   E   I   335
CAA GGG AAA AAA AGG GAC ATA CTT TCT GTG TCC ACA AGA GAT GCT GTA GAA TTA GAG ATT 1500

 I   D   *                                                                       338
ATA GAC TAA GAGGTGGAGGCAGGTTAAGTTACATGGTATTATTTAATGAAACTTACATTTTGGAAAAGAAATCTGG 1576

CATAGTAGAACCCAGTGGAAATAGTTTGAAGGTACATTGTATGACTCCTATGTTGGCTTTATTAAGTAAGGTATAGAAA 1655

TGTATTATCTTGTATGTATTCTAATGACTAGGCATCATTGTTTTAGTACCAATTCTCTTTGCCTCTATGTTATAACCCC 1734

TAAGAAGCACGCGGGACTGTTCGTCTTTAAATCAGTGGCCATTCTATCTGACTACTATGACTTTTTGTTGTTGTTCTGC 1813

TTTGGGTTTTCAGTCTGCCTGCATCAGTCTTCTCCTCTGTATACGTCTGTCTTCAACAAATGTAAGGACTAAATACCCC 1892
```

FIG. 9C

TCCCGATCACATCCATTATCAAGGATTTGAAGCCACTCCATGTACTGGGTTATAAAAGAAATGTTCTCATGAACTTTCA 1971

TGAAGTTTACATACCTTTGGGGATCTAGTCACCGAGTCACATAAAGTAAAAGTAAATGGAAAAAAAAAAAAAAAAAAA 2050

AGGGC 2055

FIG. 9D

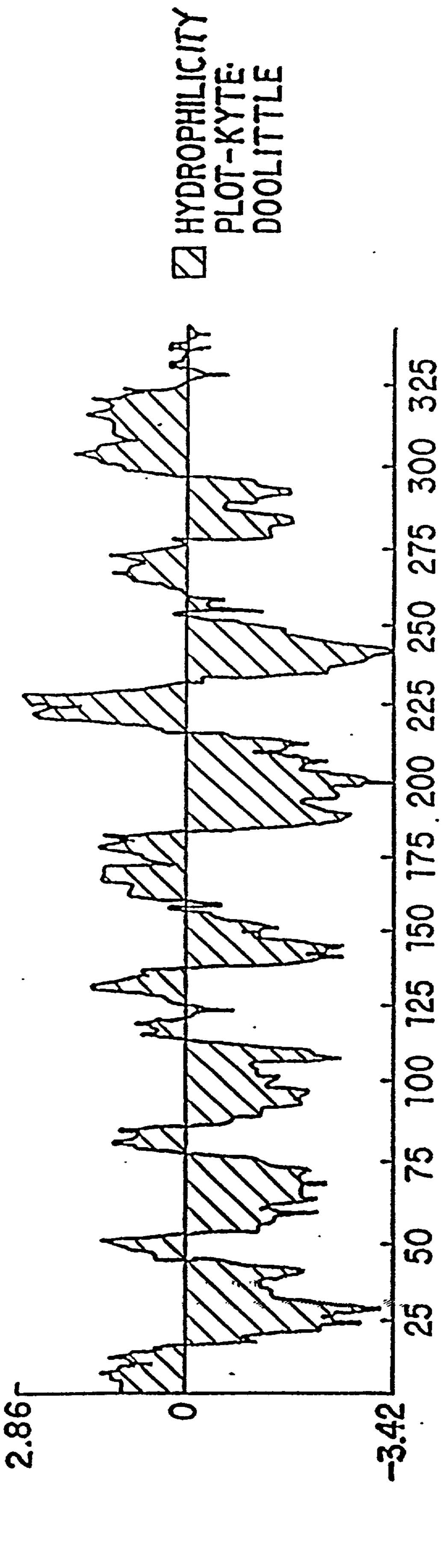

FIG. 10A

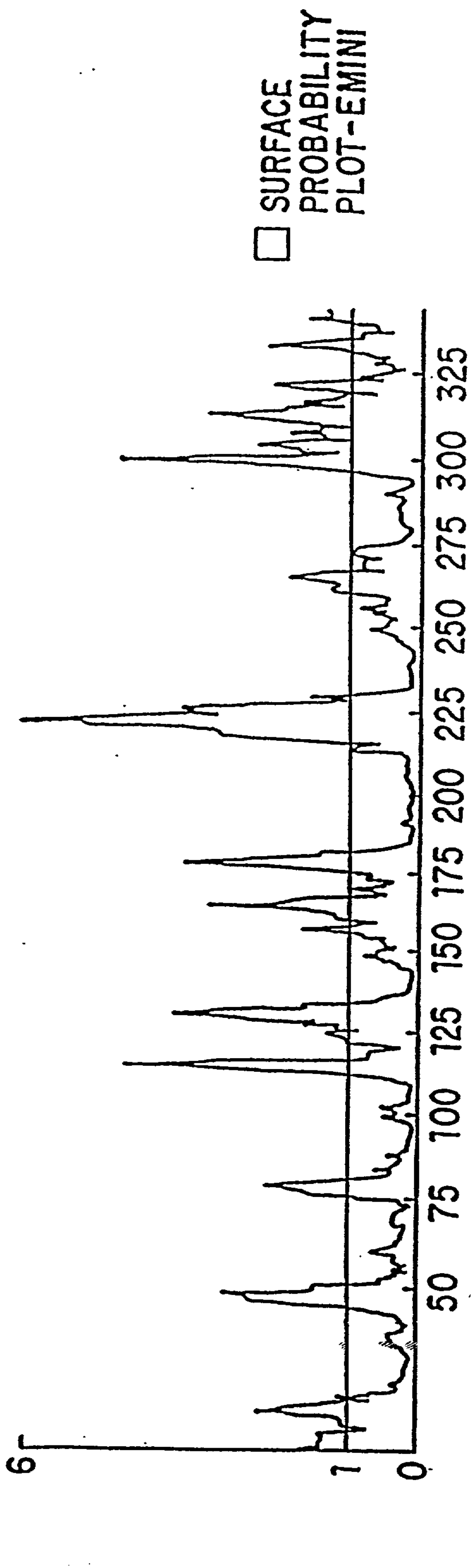

FIG. 10B

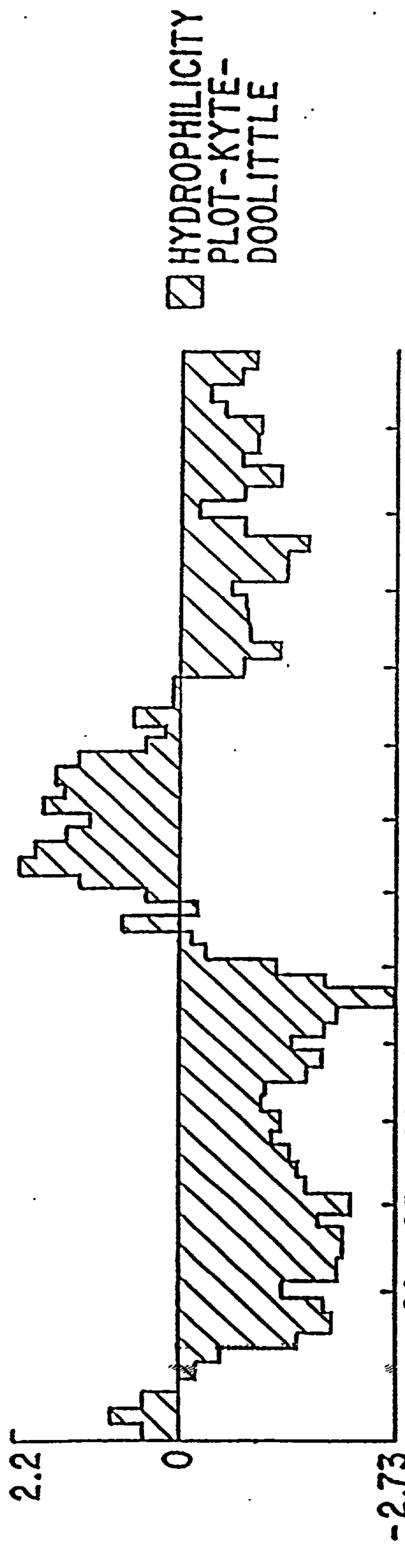

FIG. 10C

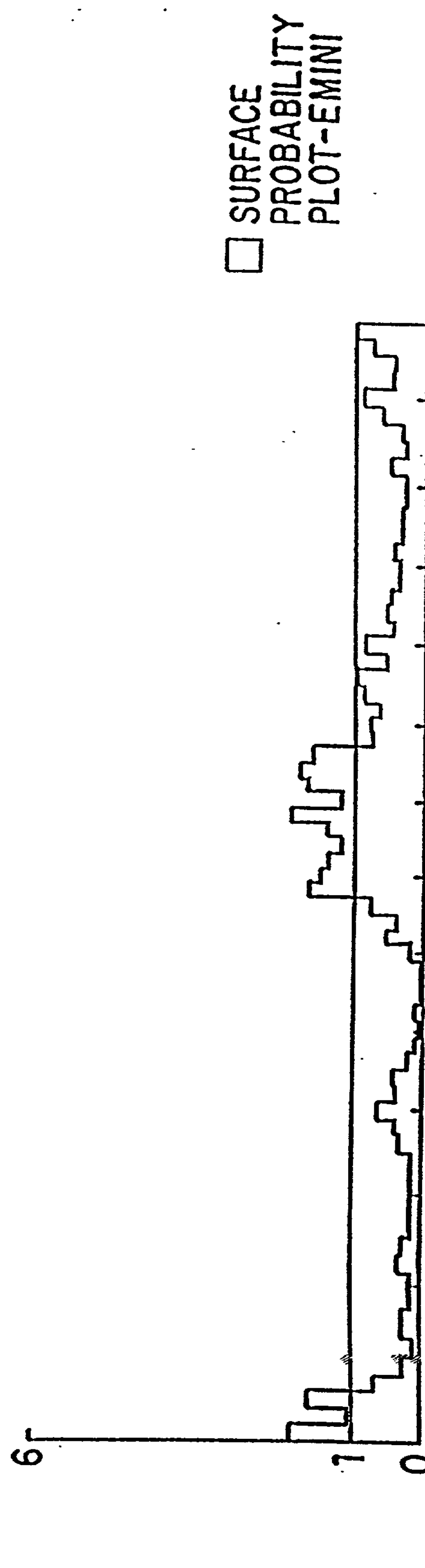

FIG. 10D

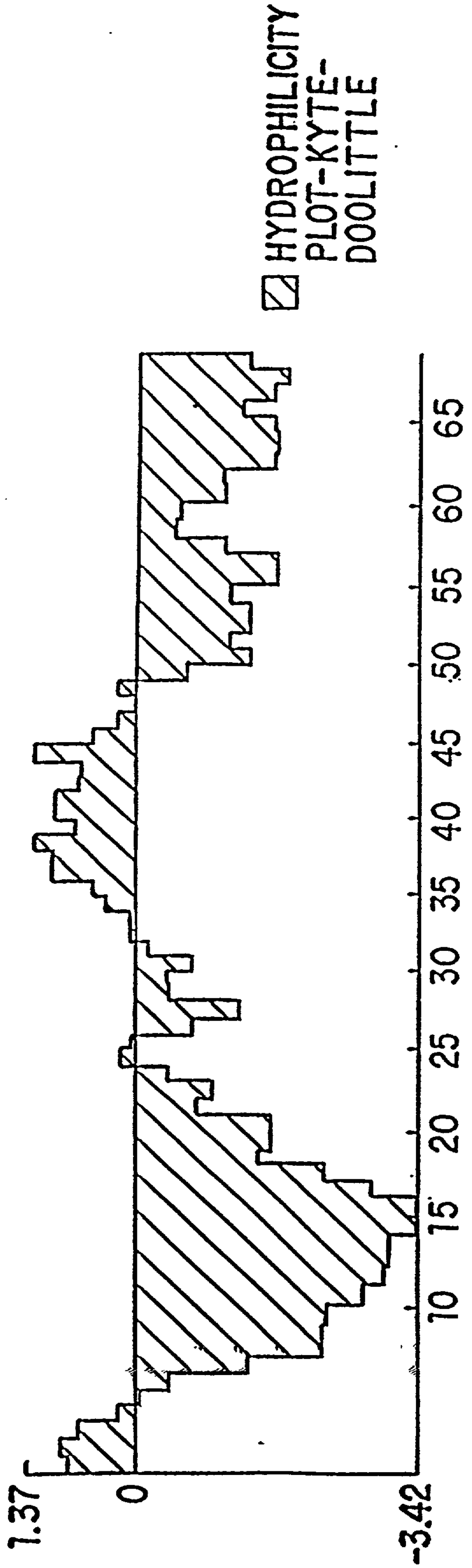

FIG. 10E

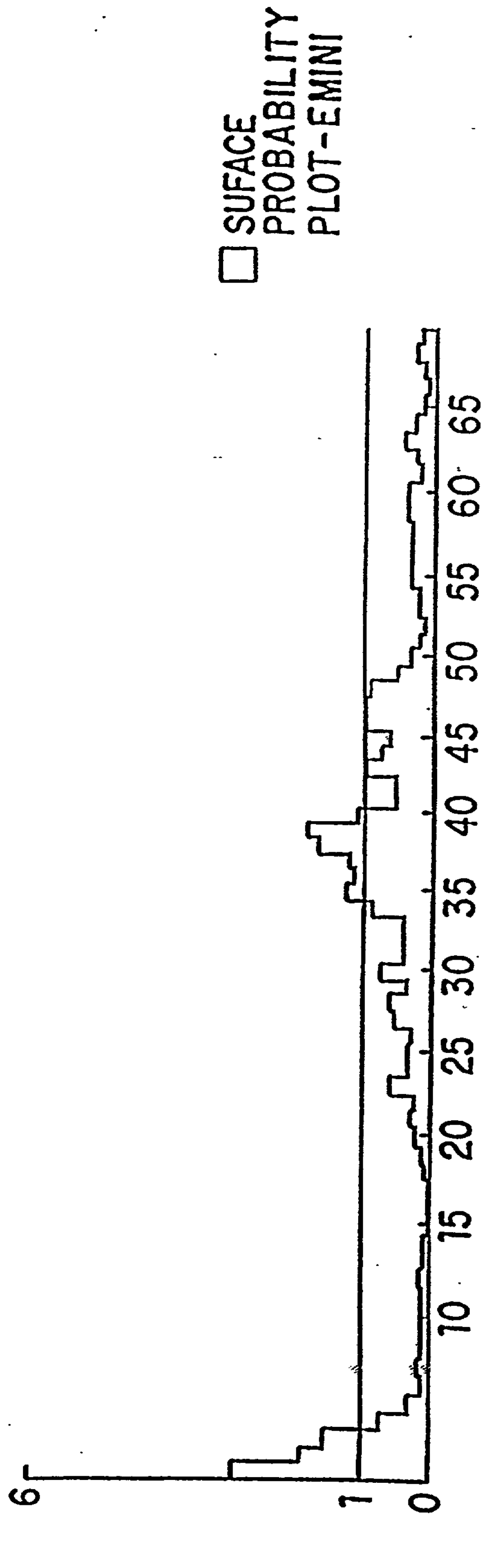

FIG. 10F

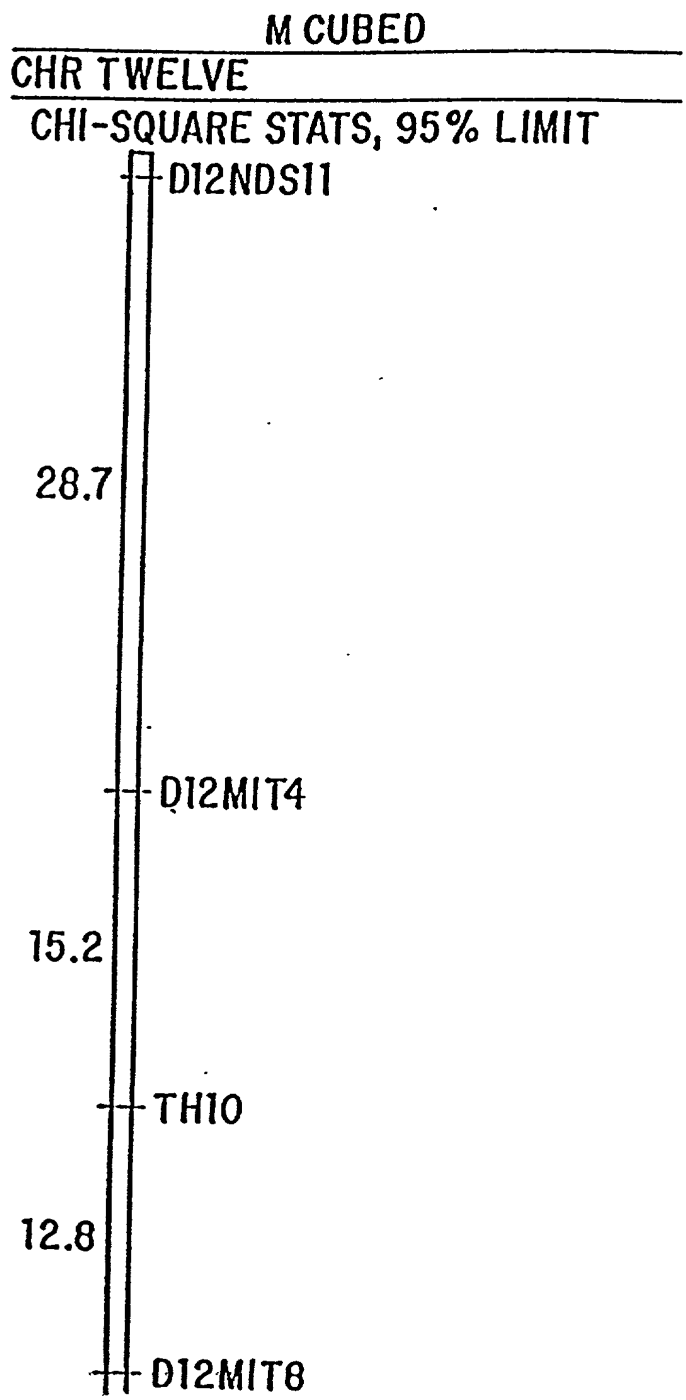
M CUBED
CHR TWELVE
CHI-SQUARE STATS, 95% LIMIT
D12NDS11
28.7
D12MIT4
15.2
TH10
12.8
D12MIT8

FIG. 11

CGCCAGTGTGCTGGAATTCGGCTTAGAGCATTTCTTTCA
AACCACAGGTTAACACACACTTACTAAAAAGCAATGCTG
TTAGAGGAGAAGGGCTTGGGAGACTCGGCCATTTGAAAC
ANAAGCAAGGCACTCTCCAGGNNCAGCAAGTGGATTCCC
ATTTCCTGCTGAGGGCGGGTTCACACTGAGACTGCACTC
CAGTCAGCGGGAGGAATCACCTGCATTAATGCTTGTCCT
CTGCAGAGCTAGTGTGCCTTCCACTCTGGGTACACTTGG
GTGTCAACATTTCAAAATGATGACCTAAGAGGCTCTCAT
AGTTGGTGATAACTATGGNAGGACAGAAGAACACTGGCT
GTATTGTCTTTTTCTTTCAGCACTAGTGTCTTGGCCCTT
AACTAAAACGGGTTCCATCATCCTCCAAACCAGGAAGAT
AGATTGTTAGACAGGTCCTTTCCCCTCAACT

FIG. 12

TTTNNGGGACAGGGTTTCNCTGTGTATCTCTGGCTGTCC
TGGAACTNACTCTGTAGACCAGGTTGGCCTCGANCTCAG
AAATCTACCTGCCTCTCCCTCCANAGTGCTGGGATTAAN
GGTGTATGCCACCAATNCCCGGCCTTAATATATTNNTAA
ACAACTTCATTTGAATGANATATTGACACTACCCTTGGA
ATAAGAGTNCCCAGAATGANGTACAGGNTTCANGGAATC
ATTTAA

FIG. 14

CTTAGCAGGTGGAGTTGCAGCAGGAAGCCTGGTAGCCAC
ACTCCAATCAGCAGGGGTCCTTGGACTCTCCACATCAAC
AAATGCCATCCTAGGGGCTGCTGGGGCACTGTTGGAGCC
TTGCTCTGAGCTTAGGAGATGACACTTCTATCAGCTCAA
CTCAAAGCCTGTACAGACTACGCAGGAGATGAAGTTCCA
AAAGGCACCTTCAGAACCCTCA

FIG. 15

```
        10         20         30         40         50         60         70
TTTTTTTTTT TNGGGAGAGG CTAGCACTGA AATTACAGTT TCAGTGGAAT TTAGAGAAGT AATAACTGCA  70
AAAATTTATT TACACACACA CACACACACA CAGGGCATTT TACCTGTGTA AGTGCAGTTT AATCANCCCC 140
ATTACCTTAT GACCTTGGTT GGCAATGTCT CTAAAGCTTT AAAATTAAAA TAAAATTAAA AAGATGGTTT 210
TCCATCTCAT AAAATCCCCT TTGGGAATGG AAGACTTCCT CTTTGGGGTN TTTTTTAGAG GGAACAGGAG 280
GTAACTGTTA ATTATTTATA CATTCTAATA AACCATGAAT GCACCACATA AAATACTGTA CTCGGGGAGC 350
AAACACTGTN TGGGGGGGTT CTCTCTTACC AGAAGGAACA GGGGGCTTTT CAATGGCTGT GGGC       414
```

FIG. 13

```
remt161g0f  F-----------------------------------------------------------      BAND 161
gi/218574/  MRQKAVSLFLCYLLLFTCSGVEAGKKKCSESSDSGSGF-WKALTFMAVGGGLAVAGLP-- CHIMP GENE
gi/32698/g  MRQKAVSVFLCYLLLFTCSGVEAGKKKCSESSDSGSGF-WKALTFMAVGGGLAVAGLP-- HUMAN 6-16
gi/32701/g  --------------------VEAGKKKCSESSDSGSGF-WKALTFMAVGGGLAVAGLP-- HUMAN 6-16
gi/32702/g  ------------------------GKKKCSESSDSGSGF-WKALTFMAVGGGLAVAGLP-- HUMAN 6-16
gi/35184/g  MEASAL----------TSSAVTSVAKVVRVASGSAVVLPLARIATVVIGGVVAMAAVPMV HUMAN P27

remt161g0f  ---FVFLA---------------------GGVAAGSLVATLQSAGVLGLSTSTNAILGAA      BAND 161
gi/218574/  --ALGFTGAGIAANSVAASLMSWSAILNGGGVPAGGLVATLQSLGAGG----SSVITGNI CHIMP GENE
gi/32698/g  --ALGFTGAGIAANSVAASLMSWSAILNGGGVPAGGLVATLQSLGAGG----SSVVIGNI HUMAN 6-16
gi/32701/g  --ALGFTGAGIAANSVAASLMSWSAILNGGGVPAGGLVATLQSLGAGG----SSVVIGNI HUMAN 6-16
gi/32702/g  --ALGFTGAGIAANSVAASLMSWSAILNGGGVPAGGLVATLQSLGAGG----SSVVIGNI HUMAN 6-16
gi/35184/g  LSAMGFTAAGIASSSIAAKMMSAAAIANGGGVASGSLVGTLQSLGATGLSGLTKFILGSI HUMAM P27

remt161g0f  GALLEPCSELRR-------       BAND 161
gi/218574/  GALMGYATHKYLDSEEDEE  CHIMP GENE
gi/32698/g  GALMRYATHKYLDSEEDEE  HUMAN 6-16
gi/32701/g  GALMRYATHKYLDSEEDEE  HUMAN 6-16
gi/32702/g  GALMRYATHKYLDSEEDEE  HUMAN 6-16
gi/35184/g  GSAIAAVIARFY         HUMAN P27
```

FIG. 16

```
                                         M   F   S   G   L   T   L     6
NGTCGACCCACGCGTCCGGATTTCCCCTCCCAAGTACTC ATG TTT TCA GGT CTT ACC CTC   60

 N   C   V   L   L   L   L   Q   L   L   L   A   R   S   L   E   D   G   Y   K    26
AAC TGT GTC CTG CTG CTG CTG CAA CTA CTA CTT GCA AGG TCA TTG GAA GAT GGT TAT AAG  120

 V   E   V   G   K   N   A   Y   L   P   C   S   Y   T   L   P   T   S   G   T    46
GTT GAG GTT GGT AAA AAT GCC TAT CTG CCC TGC AGT TAC ACT CTA CCT ACA TCT GGG ACA  180

 L   V   P   M   C   W   G   K   G   F   C   P   W   S   Q   C   T   N   E   L    66
CTT GTG CCT ATG TGC TGG GGC AAG GGA TTC TGT CCT TGG TCA CAG TGT ACC AAT GAG TTG  240

 L   R   T   D   E   R   N   V   T   Y   Q   K   S   S   R   Y   Q   L   K   G    86
CTC AGA ACT GAT GAA AGA AAT GTG ACA TAT CAG AAA TCC AGC AGA TAC CAG CTA AAG GGC  300

 D   L   N   K   G   D   V   S   L   I   I   K   N   V   T   L   D   D   H   G   106
GAT CTC AAC AAA GGA GAT GTG TCT CTG ATC ATA AAG AAT GTG ACT CTG GAT GAC CAT GGG  360

 T   Y   C   C   R   I   Q   F   P   G   L   M   N   D   K   K   L   E   L   K   126
ACC TAC TGC TGC AGG ATA CAG TTC CCT GGT CTT ATG AAT GAT AAA AAA TTA GAA CTG AAA  420

 L   D   I   K   A   A   K   V   T   P   A   Q   T   A   H   G   D   S   T   T   146
TTA GAC ATC AAA GCA GCC AAG GTC ACT CCA GCT CAG ACT GCC CAT GGG GAC TCT ACT ACA  480

 A   S   P   R   T   L   T   T   E   R   N   G   S   E   T   Q   T   L   V   T   166
GCT TCT CCA AGA ACC CTA ACC ACG GAG AGA AAT GGT TCA GAG ACA CAG ACA CTG GTG ACC  540
```

FIG. 17A

```
 L   H   N   N   N   G   T   K   I   S   T   W   A   D   E   I   K   D   S   G   186
CTC CAT AAT AAC AAT GGA ACA AAA ATT TCC ACA TGG GCT GAT GAA ATT AAG GAC TCT GGA  600

 E   T   I   R   T   A   I   H   I   G   V   G   V   S   A   G   L   T   L   A   206
GAA ACG ATC AGA ACT GCT ATC CAC ATT GGA GTG GGA GTC TCT GCT GGG TTG ACC CTG GCA  660

 L   I   I   G   V   L   I   L   K   W   Y   S   C   K   K   K   K   L   S   S   226
CTT ATC ATT GGT GTC TTA ATC CTT AAA TGG TAT TCC TGT AAG AAA AAG AAG TTA TCG AGT  720

 L   S   L   I   T   L   A   N   L   P   P   G   G   L   A   N   A   G   A   V   246
TTG AGC CTT ATT ACA CTG GCC AAC TTG CCT CCA GGA GGG TTG GCA AAT GCA GGA GCA GTC  780

 R   I   R   S   E   E   N   I   Y   T   I   E   E   N   V   Y   E   V   E   N   266
AGG ATT CGC TCT GAG GAA AAT ATC TAC ACC ATC GAG GAG AAC GTA TAT GAA GTG GAG AAT  840

 S   N   E   Y   Y   C   Y   V   N   S   Q   Q   P   S   *                       280
TCA AAT GAG TAC TAC TGC TAC GTC AAC AGC CAG CAG CCA TCC TGA CCGCCTCTGGACTGCCACT  903

TTTAAAGGCTCGCCTTCATTTCTGACTTTGGTATTTCCCTTTKTGGAAAACTATGTGATATGTCACTTGGCAACCTCAT  982

TGGAGGTTCTGACCACAGCCACTGAGAAAAGAGTTCCAGTTTTCTGGGGATAATTAACTCACAAGGGGATTCGACTGTA 1061

ACTCATGCTACATTGAAATGCTCCATTTTATCCCTGAGTTTCAGGGATCGGATCTCCCACTCCAGAGACTTCAATCATG 1140

CGTGTTGAAGCTCACTCGTGCTTTCATACATTAGGAATGGTTAGTGTGATGTCTTTGAGACATAGAGGTTTGTGGTATA 1219
```

FIG. 17B

TCCGCAAAGCTCCTGAACAGGTAGGGGGAATAAAGGGCTAAGATAGGAAGGTGCGGYTCTTTGTTGATGTTGGAAAATC 1298

TTAAAGAAGTTGGTAGCTTTTCT AGAGATTTCTGACCTTGAAAGATTAAGAAAAAGCCAGGTGGCATATGCTTAACAC 1376

GATATAACTTGGGAACCTTAGGCAGGAGGGTGATAAGTTCAAGGTCAGCCAGGGCTATGCTGGTAAGACTGTCTCAMCA 1455

TCCAAAGACGAAAATAAACATAGAGACAGCAGGAGGCTGGAGATGAGGCTCGGACAGTGAGGTGCATTGTGTACAAGCA 1534

CGAGGAATCTATATTTGATCGTAGACCCCACATGAAAAAGCTAGGCCTGGTAGAGCATGCTTGTAGACTCAAGAGATGG 1613

AGAGGTAAAGGCACAACAGATCCCCGGGGCTTGCGTGCAGTCAGCTTAGCCTAGGTGCTGAGTTCCAAGTCCACAAGAG 1692

TCCCTGTCTCAMAGTAAGATGGRCTGAGTATCTGGCGCATGTCCATGGGGGTTGTCCTCTCCTCTCAGAAGAGACATGC 1771

ACATGACCCTGCACACACACACACACACACACACACACACACACACACACACACATGAAATGAAGGTTCTCTCTG 1850

TGCCTGCTACCTCTCTATAACATGTATCTCTACAGGACTCTCCTCTGCCTCTGTTAAGACATGAGTGGGAGCATGGCAG 1929

AGCAGTCCAGTAATTTATTCCAGCACTCAGAAGGCTGGAGCAGAAGCGTGGAGAGTTCAGGAGCACTGTGCCCAACACT 2008

GCCAGACTCTTCTTACACAAGAAAAAGGTTACCCGCAAGCAGCCTGCTGTCTGTAAAAGGAAACCCTGCGAAAGGCAAA 2087

CTTTGACTGTTGTGTGCTCAAGGGGAACTGACTCAGACAACTTCTCCATTCCTGGAGGAAACTGGAGCTGTTTCTGACA 2166

GAAGAACAACCGGTGACTGGGACATACGAAGGCAGAGCTCTTGCAGCAATCTATATAGTCAGCAAAATATTCTTTGGGA 2245

FIG. 17C

GGACAGTCGTCACCAAATTGATTTCCAAGCCGGTGGACCTCAGTTTCATCTGGCTTACAGCTGCCTGCCCAGTGCCCTT 2324

GATCTGTGCTGGCTCCCATCTATAACAGAATCAAATTAAATAGACCCCGAGTGAAAATATTAAGTGAGCAGAAAGGTAG 2403

CTTTGTTCAAAGATTTTTTTGCATTGGGGAGCAACTGTGTACATCAGAGGACATCTGTTAGTGAGGACACCAAAACCTG 2482

TGGTACCGTTTTTTCATGTATGAATTTTGTTGTTTAGGTTGCTTCTAGCTAGCTGTGGAGGTCCTGGCTTTCTTAGGTG 2561

GGTATGGAAGGGAGACCATCTAACAAAATCCATTAGAGATAACAGCTCTCATGCAGAAGGGAAAACTAATCTCAAATGT 2640

TTTAAAGTAATAAAACTGTACTGGCAAAGTACTTTGAGCATAAAAAAAAAAAAAAAAAAAGGGCGGCCGC 2710

FIG. 17D

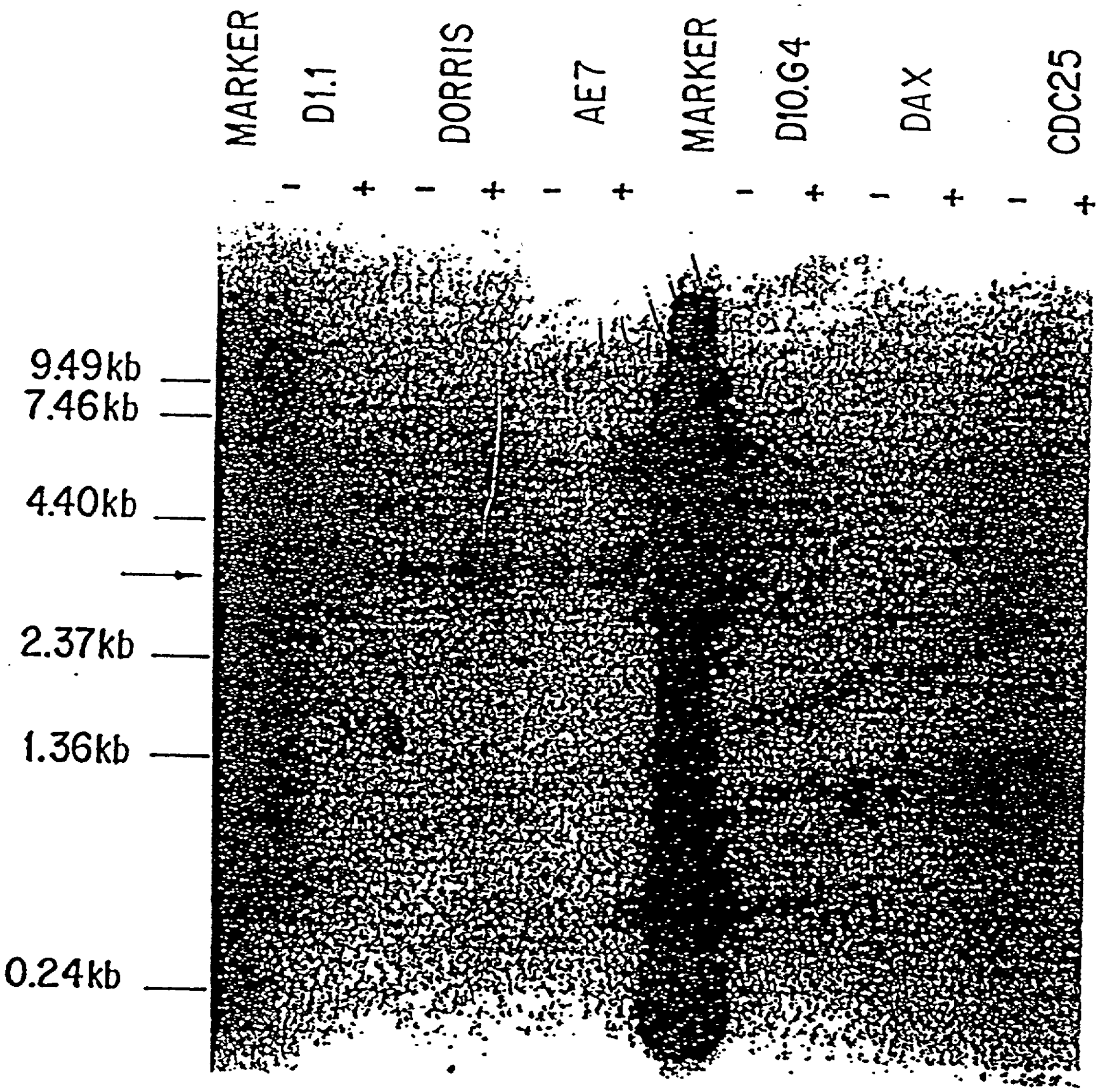
MARKER
DI.1
DORRIS
AE7
MARKER
DIO.G4
DAX
CDC25
- + - + - + - + - + - +
9.49kb
7.46kb
4.40kb
2.37kb
1.36kb
0.24kb

FIG. 18

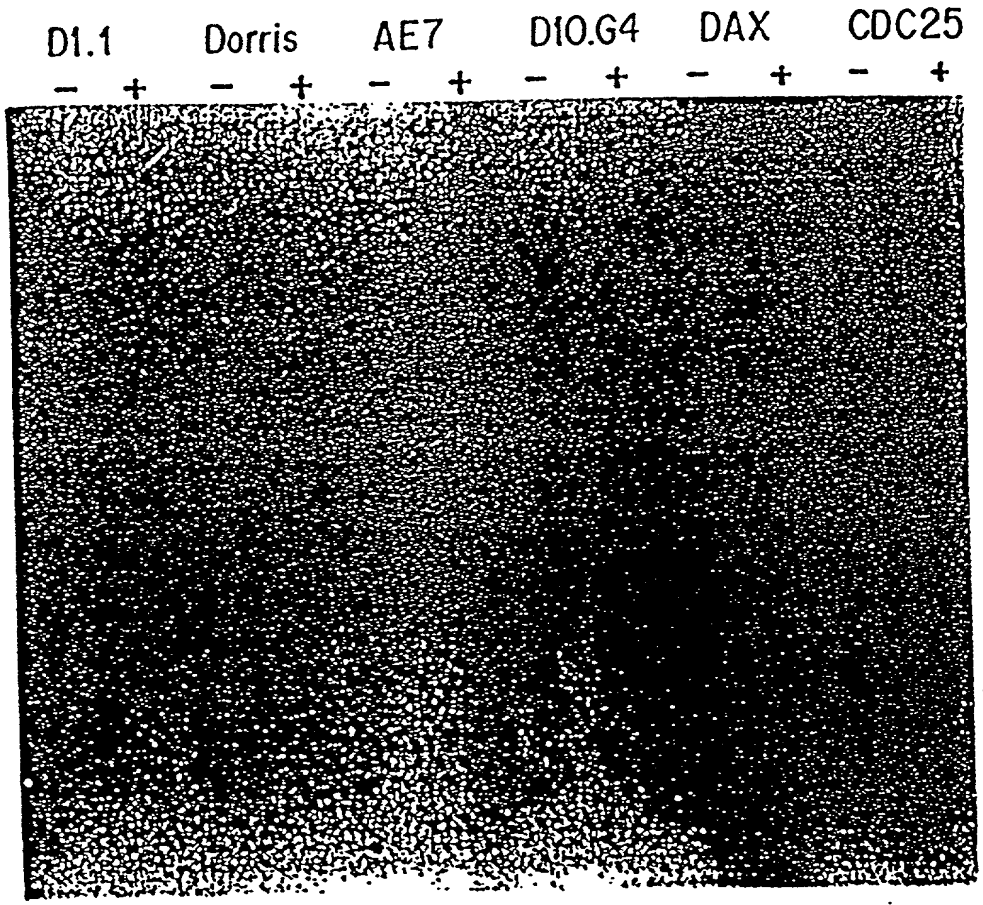

FIG. 19

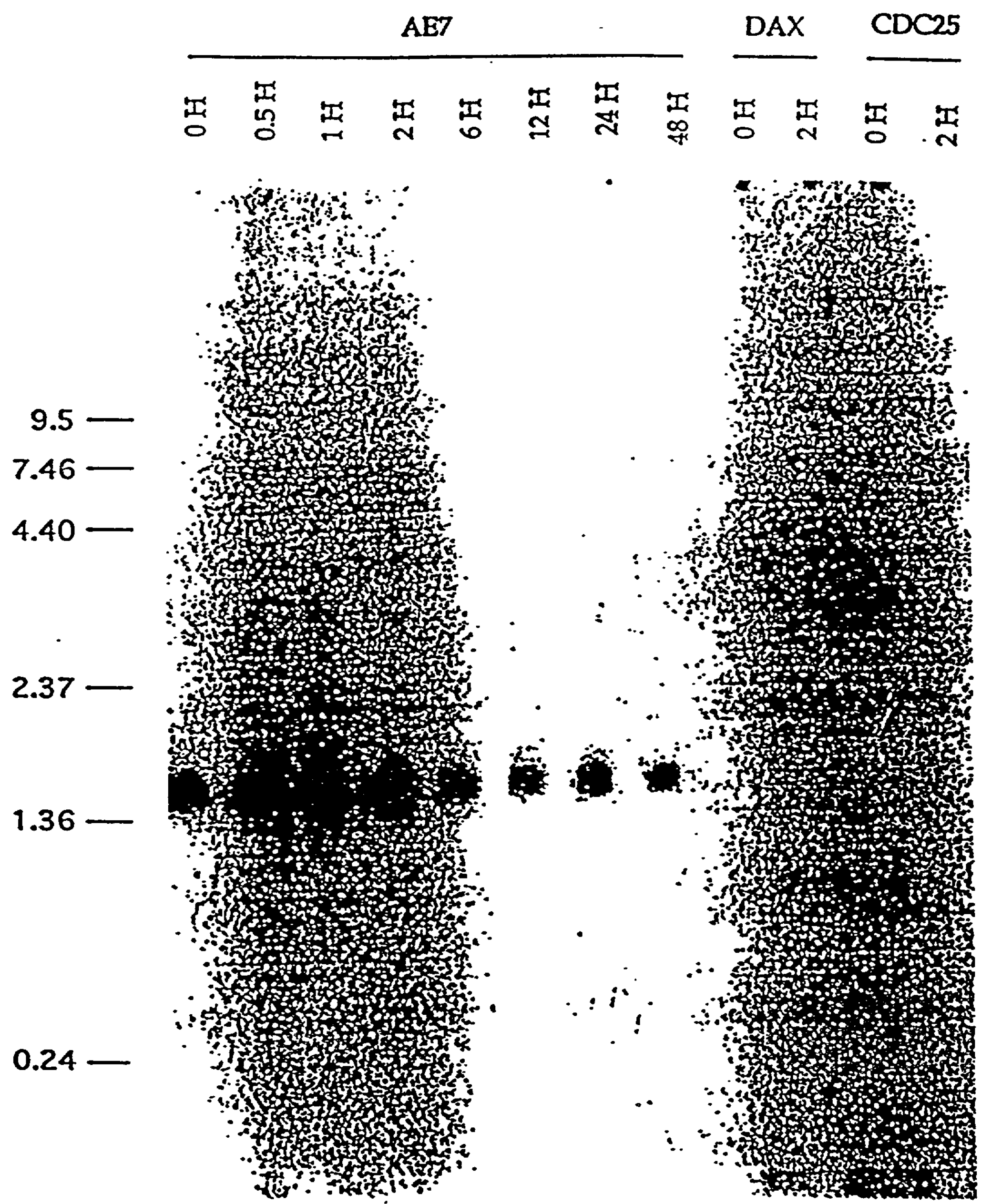
AE7
DAX
CDC25
0 H
0.5 H
1 H
2 H
6 H
12 H
24 H
48 H
0 H
2 H
0 H
2 H
9.5
7.46
4.40
2.37
1.36
0.24

FIG. 20

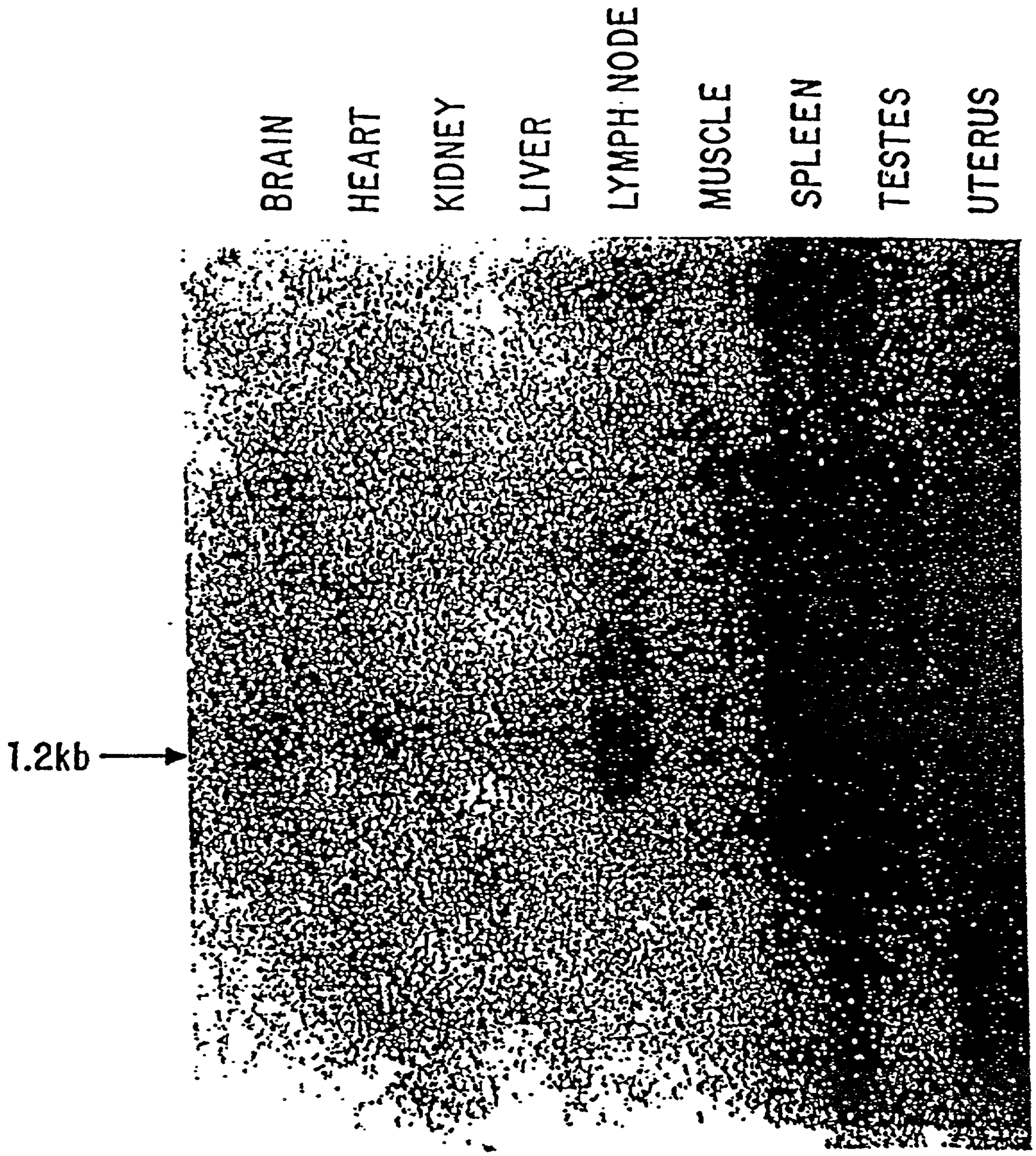
BRAIN
HEART
KIDNEY
LIVER
LYMPH NODE
MUSCLE
SPLEEN
TESTES
UTERUS
1.2kb

FIG. 21

```
                                M   T   L   T   A   H   L   S   Y   F   L   V   L    13
C CGGGTCGACC CACGCGTCCG ATG ACA CTG ACT GCC CAC CTC TCC TAC TTT CTG GTC CTG    60

 L   L   A   G   Q   G   L   S   D   S   L   L   T   K   D   A   G   P   R   P    33
TTG TTA GCG GGC CAA GGC CTC AGT GAC TCC CTC CTC ACC AAG GAT GCA GGT CCC CGC CCA   120

 L   E   L   K   E   V   F   K   L   F   Q   I   R   F   N   R   S   Y   W   N    53
CTG GAG CTG AAG GAA GTC TTC AAG CTG TTC CAG ATC CGG TTC AAC CGG AGT TAC TGG AAC   180

 P   A   E   Y   T   R   R   L   S   I   F   A   H   N   L   A   Q   A   Q   R    73
CCA GCA GAG TAC ACT CGC CGT CTG AGC ATC TTT GCC CAC AAT CTG GCT CAG GCT CAA AGG   240

 L   Q   Q   E   D   L   G   T   A   E   F   G   E   T   P   F   S   D   L   T    93
CTA CAG CAA GAA GAC TTG GGT ACA GCT GAG TTT GGA GAG ACT CCA TTC AGT GAC CTC ACA   300

 E   E   E   F   G   Q   L   Y   G   Q   E   R   S   P   E   R   T   P   N   M   113
GAG GAG GAG TTT GGC CAG TTA TAC GGG CAG GAG AGG TCA CCA GAA AGG ACC CCC AAC ATG   360

 T   K   K   V   E   S   N   T   W   G   E   S   V   P   R   T   C   D   W   R   133
ACC AAA AAG GTA GAG TCT AAC ACG TGG GGG GAA TCT GTG CCC CGC ACC TGT GAC TGG CGT   420

 K   A   K   N   I   I   S   S   V   K   N   Q   G   S   C   K   C   C   W   A   153
AAA GCA AAG AAC ATC ATC TCG TCG GTC AAG AAC CAG GGA AGC TGC AAA TGC TGC TGG GCC   480

 M   A   A   A   D   N   I   Q   A   L   W   R   I   K   H   Q   Q   F   V   D   173
ATG GCA GCT GCC GAC AAC ATC CAG GCT CTG TGG CGC ATC AAA CAC CAG CAG TTT GTG GAC   540
```

FIG. 22A

V S V Q E L L D C E R C G N G C N G G F 193
GTG TCT GTG CAG GAG CTG CTG GAC TGC GAA CGC TGT GGA AAT GGT TGC AAT GGT GGC TTC 600

V W D A Y L T V L N N S G L A S E K D Y 213
GTG TGG GAC GCA TAT CTA ACT GTC CTC AAC AAC AGT GGC CTG GCC AGT GAA AAG GAT TAT 660

P F Q G D R K P H R C L A K K Y K K V A 233
CCA TTC CAG GGG GAC AGA AAG CCT CAC AGA TGC CTA GCC AAG AAG TAC AAG AAG GTG GCC 720

W I Q D F T M L S N N E Q A I A H Y L A 253
TGG ATC CAG GAT TTC ACC ATG TTG TCC AAT AAT GAG CAG GCA ATT GCC CAC TAC CTG GCC 780

V H G P I T V T I N M K L L Q H Y Q K G 273
GTG CAT GGA CCT ATC ACC GTG ACC ATC AAC ATG AAA CTA CTC CAG CAT TAC CAG AAG GGT 840

V I K A T P S S C D P R Q V D H S V L L 293
GTC ATC AAG GCT ACA CCC AGC TCC TGT GAC CCT CGG CAA GTG GAC CAC TCT GTC TTG CTG 900

V G F G K E K E G M Q T G T V L S H S R 313
GTG GGC TTT GGC AAG GAG AAA GAG GGC ATG CAG ACA GGG ACA GTC TTG TCC CAT TCT CGA 960

K R R H S S P Y W I L K N S W G A H W G 333
AAA CGT CGC CAC TCC TCC CCA TAC TGG ATC CTG AAG AAC TCC TGG GGA GCT CAC TGG GGC 1020

E K G Y F R L Y R G N N T C G V T K Y P 353
GAG AAG GGT TAC TTC AGG CTG TAT CGG GGA AAC AAC ACC TGT GGA GTC ACC AAG TAT CCC 1080

FIG. 22B

```
 F   T   A   Q   V   D   S   P   V   K   K   A   R   T   S   C   P   P   *       371
TTC ACA GCT CAA GTG GAC TCA CCA GTA AAG AAG GCA CGG ACC TCT TGT CCT CCC TGA AGG 1140

CAGCAGVCAC TCTTCTGCTT CTCCCACATG GCCACTGCCC CTTGTCAGCC CTGCCCACAT CCTCTCTGTA    1210

TGGCTTCATA AACCAAGACT GCTCCGTGAA AAAAAAAAAAAAAAAAA                              1257
```

FIG. 22C

Pre-Pro

```
                                M   T   L   T   A   H   L   S   Y   F   L   V   L    13
C CGGGTCGACC CACGCGTCCG ATG ACA CTG ACT GCC CAC CTC TCC TAC TTT CTG GTC CTG    60

L   L   A   G   Q   G   L   S   D   S   L   L   T   K   D   A   G   P   R   P    33
TTG TTA GCG GGC CAA GGC CTC AGT GAC TCC CTC CTC ACC AAG GAT GCA GGT CCC CGC CCA  120

L   E   L   K   E   V   F   K   L   F   Q   I   R   F   N   R   S   Y   W   N    53
CTG GAG CTG AAG GAA GTC TTC AAG CTG TTC CAG ATC CGG TTC AAC CGG AGT TAC TGG AAC  180

P   A   E   Y   T   R   R   L   S   I   F   A   H   N   L   A   Q   A   Q   R    73
CCA GCA GAG TAC ACT CGC CGT CTG AGC ATC TTT GCC CAC AAT CTG GCT CAG GCT CAA AGG  240

L   Q   Q   E   D   L   G   T   A   E   F   G   E   T   P   F   S   D   L   T    93
CTA CAG CAA GAA GAC TTG GGT ACA GCT GAG TTT GGA GAG ACT CCA TTC AGT GAC CTC ACA  300

E   E   E   F   G   Q   L   Y   G   Q   E   R   S   P   E   R   T   P   N   M   113
GAG GAG GAG TTT GGC CAG TTA TAC GGG CAG GAG AGG TCA CCA GAA AGG ACC CCC AAC ATG  360

T   K   K   V   E   S   N   T   W   G   E   S   V   P   R   T   C   D   W   R   133
ACC AAA AAG GTA GAG TCT AAC ACG TGG GGG GAA TCT GTG CCC CGC ACC TGT GAC TGG CGT  420

K   A   K   N   I   I   S   S   V   K   N   Q   G   S   C   K   C   C   W   A   153
AAA GCA AAG AAC ATC ATC TCG TCG GTC AAG AAC CAG GGA AGC TGC AAA TGC TGC TGG GCC  480

M   A   A   A   D   N   I   Q   A   L   W   R   I   K   H   Q   Q   F   V   D   173
ATG GCA GCT GCC GAC AAC ATC CAG GCT CTG TGG CGC ATC AAA CAC CAG CAG TTT GTG GAC  540
```

FIG.23A

MATURE

```
V   S   V   Q   E   L   L   D   C   E   R   C   G   N   G   C   N   G   G   F    193
GTC TCT GTG CAG GAG CTG CTG GAC TGC GAA CGC TGT GGA AAT GGT TGC AAT GGT GGC TTC  600

V   W   D   A   Y   L   T   V   L   N   N   S   G   L   A   S   E   K   D   Y    213
GTG TGG GAC GCA TAT CTA ACT GTC CTC AAC AAC AGT GGC CTG GCC AGT GAA AAG GAT TAT  660

P   F   Q   G   D   R   K   P   H   R   C   L   A   K   K   Y   K   K   V   A    233
CCA TTC CAG GGG GAC AGA AAG CCT CAC AGA TGC CTA GCC AAG AAG TAC AAG AAG GTG GCC  720

W   I   Q   D   F   T   M   L   S   N   N   E   Q   A   I   A   H   Y   L   A    253
TGG ATC CAG GAT TTC ACC ATG TTG TCC AAT AAT GAG CAG GCA ATT GCC CAC TAC CTG GCC  780

V   H   G   P   I   T   V   T   I   N   M   K   L   L   Q   H   Y   Q   K   G    273
GTG CAT GGA CCT ATC ACC GTG ACC ATC AAC ATG AAA CTA CTC CAG CAT TAC CAG AAG GGT  840

V   I   K   A   T   P   S   S   C   D   P   R   Q   V   D   H   S   V   L   L    293
GTC ATC AAG GCT ACA CCC AGC TCC TGT GAC CCT CGG CAA GTG GAC CAC TCT GTC TTG CTG  900

V   G   F   G   K   E   K   E   G   M   Q   T   G   T   V   L   S   H   S   R    313
GTG GGC TTT GGC AAG GAG AAA GAG GGC ATG CAG ACA GGG ACA GTC TTG TCC CAT TCT CGA  960

K   R   R   H   S   S   P   Y   W   I   L   K   N   S   W   G   A   H   W   G    333
AAA CGT CGC CAC TCC TCC CCA TAC TGG ATC CTG AAG AAC TCC TGG GGA GCT CAC TGG GGC 1020
```

FIG.23B

```
E   K   G   Y   F   R   L   Y   R   G   N   N   T   C   G   V   T   K   Y   P    353
GAG AAG GGT TAC TTC AGG CTG TAT CGG GGA AAC AAC ACC TGT GGA GTC ACC AAG TAT CCC 1080

F   T   A   Q   V   D   S   P   V   K   K   A   R   T   S   C   P   P   *        371
TTC ACA GCT CAA GTG GAC TCA CCA GTA AAG AAG GCA CGG ACC TCT TGT CCT CCC TGA AGG 1140

CAGCAGVCAC TCTTCTGCTT CTCCCACATG GCCACTGCCC CTTGTCAGCC CTGCCCACAT CCTCTCTGTA     1210

TGGCTTCATA AACCAAGACT GCTCCGTGAA AAAAAAAAAAAAAAAAA                             1257
```

FIG.23C

```
                                         M   F   S   H   L   P      6
CGCTAACAGAGGTGTCCTCTGACTTTTCTTCTGCAAGCTCC ATG TTT TCA CAT CTT CCC  18

 F   D   C   V   L   L   L   L   L   L   L   T   R   S   S   E   V   E   Y     26
TTT GAC TGT GTC CTG CTG CTG CTG CTG CTA CTA CTT ACA AGG TCC TCA GAA GTG GAA TAC  78

 R   A   E   V   G   Q   N   A   Y   L   P   C   F   Y   T   P   A   A   P   G     46
AGA GCG GAG GTC GGT CAG AAT GCC TAT CTG CCC TGC TTC TAC ACC CCA GCC GCC CCA GGG 138

 N   L   V   P   V   C   W   G   K   G   A   C   P   V   F   E   C   G   N   V     66
AAC CTC GTG CCC GTC TGC TGG GGC AAA GGA GCC TGT CCT GTG TTT GAA TGT GGC AAC GTG 198

 V   L   R   T   D   E   R   D   V   N   Y   W   T   S   R   Y   W   L   N   G     86
GTG CTC AGG ACT GAT GAA AGG GAT GTG AAT TAT TGG ACA TCC AGA TAC TGG CTA AAT GGG 258

 D   F   R   K   G   D   V   S   L   T   I   E   N   V   T   L   A   D   S   G    106
GAT TTC CGC AAA GGA GAT GTG TCC CTG ACC ATA GAG AAT GTG ACT CTA GCA GAC AGT GGG 318

 I   Y   C   C   R   I   Q   I   P   G   I   M   N   D   E   K   F   N   L   K    126
ATC TAC TGC TGC CGG ATC CAA ATC CCA GGC ATA ATG AAT GAT GAA AAA TTT AAC CTG AAG 378

 L   V   I   K   P   A   K   V   T   P   A   P   T   L   Q   R   D   F   T   A    146
TTG GTC ATC AAA CCA GCC AAG GTC ACC CCT GCA CCG ACT CTG CAG AGA GAC TTC ACT GCA 438

 A   F   P   R   M   L   T   T   R   G   H   G   P   A   E   T   Q   T   L   G    166
GCC TTT CCA AGG ATG CTT ACC ACC AGG GGA CAT GGC CCA GCA GAG ACA CAG ACA CTG GGG 498

 S   L   P   D   I   N   L   T   Q   I   S   T   L   A   N   E   L   R   D   S    186
AGC CTC CCT GAT ATA AAT CTA ACA CAA ATA TCC ACA TTG GCC AAT GAG TTA CGG GAC TCT 558

 R   L   A   N   D   L   R   D   S   G   A   T   I   R   I   G   I   Y   I   G    206
AGA TTG GCC AAT GAC TTA CGG GAC TCT GGA GCA ACC ATC AGA ATA GGC ATC TAC ATC GGA 618

 A   G   I   C   A   G   L   A   L   A   L   I   F   G   A   L   I   F   K   W    226
GCA GGG ATC TGT GCT GGG CTG GCT CTG GCT CTT ATC TTC GGC GCT TTA ATT TTC AAA TGG 678

 Y   S   H   S   K   E   K   I   Q   N   L   S   L   I   S   L   A   N   L   P    246
TAT TCT CAT AGC AAA GAG AAG ATA CAG AAT TTA AGC CTC ATC TCT TTG GCC AAC CTC CCT 738

 P   S   G   L   A   N   A   V   A   E   G   I   R   S   E   E   N   I   Y   T    266
CCC TCA GGA TTG GCA AAT GCA GTA GCA GAG GGA ATT CGC TCA GAA GAA AAC ATC TAT ACC 798

 I   E   E   N   V   Y   E   V   E   E   P   N   E   Y   Y   C   Y   V   S   S    286
ATT GAA GAG AAC GTA TAT GAA GTG GAG GAG CCC AAT GAG TAT TAT TGC TAT GTC AGC AGC 858

 R   Q   Q   P   S   Q   P   L   G   C   R   F   A   M   P                        301
AGG CAG CAA CCC TCA CAA CCT TTG GGT TGT CGC TTT GCA ATG CCA TAGATCCAACCACCTTATT 903

TTTGAGCTTGGTGTTTTGTCTTTTTCAGAAACTATGAGCTGTGTCACCTGACTGGTTTTGGAGGTTCTGTCCACTGCTA
TGGAGCAGAGTTTTCCCATTTTCAGAAGATAATGACTCACATGGGAATTGAACTGGGACCTGCACTGAACTTAAACAGG
CATGTCATTGCCTCTGTATTTAAGCCAACAGAGTTACCCAACCCAGAGACTGTTAATCATGGATGTTAGAGCTCAAACG
GGCTTTTATATACACTAGGAATTCTTGACGTGGGGTCTCTGGAGCTCCAGGAAATTCGGG CACATCATATGTCCATGA
AACTTCAGATAAACTAGGRAAAACTGGGTGCTGAGGTGAAAGCATAACTTTTTTGGCACAGAAAGTCTAAAGGGGCCAC
TGATTTTCAAAGAGATCTGTGATCCCTTTTTGTTTTTTGTTTTTGAGATGGAGTCTTGCTCTGTTGCCCAGGCTGGAGT
GCAATGGCACAATCTCGGCTCACTGCAAGCTCCGCCTCCTGGGTTCAAGCGATTCTCCTGCCTCAGCCTCCTGAGTGGC
TGGGATTACAGGCATGCACCACCATGCCCAGCTAATTTGTTGTATTTTTAGTAGAGACAGGGTTTCACCATGTTGGCCA
```

FIG. 24

GTGTGGTCTCAAACTCCTGACCTCATGATTTGCCTGCCTCGGCCTCCCAAAGCACTGGGATTACAGGCGTGAGCCACCA

CATCCAGCCAGTGATCCTTAAAAGATTAAGAGATGACTGGACTAGGTCTACCTTGATCTTGAAGATTCCCTTGGAATGT

TGAGATTTAGGCTTATTTGAGCACTACCTGCCCAACTGTCAGTGCCAGTGCATAGCCCTTCTTTTGTCTCCCTTATGAA

GACTGCCCTGCAGGGCTGAGATGTGGCAGGAGCTCCCAGGGAAAAAGGAAGTGCATTTGATTGGTGTGTATTGGCCAAG

TTTTGCTTGTTGTGTGCTTGAAAGAAAATATCTCTGACCAACTTCTGTATTCGTGGACCAAACTGAAGCTATATTTTTC

ACAGAAGAAGAAGCAGTGACGGGGACACAAATTCTGTTGCCTGGTGGAAAGAAGGCAAAGGCCTTCAGCAATCTATATT

ACCAGCGCTGGATCCTTTGACAGAGAGTGGTCCCTAAACTTAAATTTCAAGACGGTATAGGCTTGATCTGTCTTGCTTA

TTGTTGCCCCCTGCGCCTAGCACAATTCTGACACACAATTGGAACTTACTAAAAATTTTTTTTTACTGTTAAAAAAAAA

AAAAAAAAAA

FIG. 24 (cont'd.)

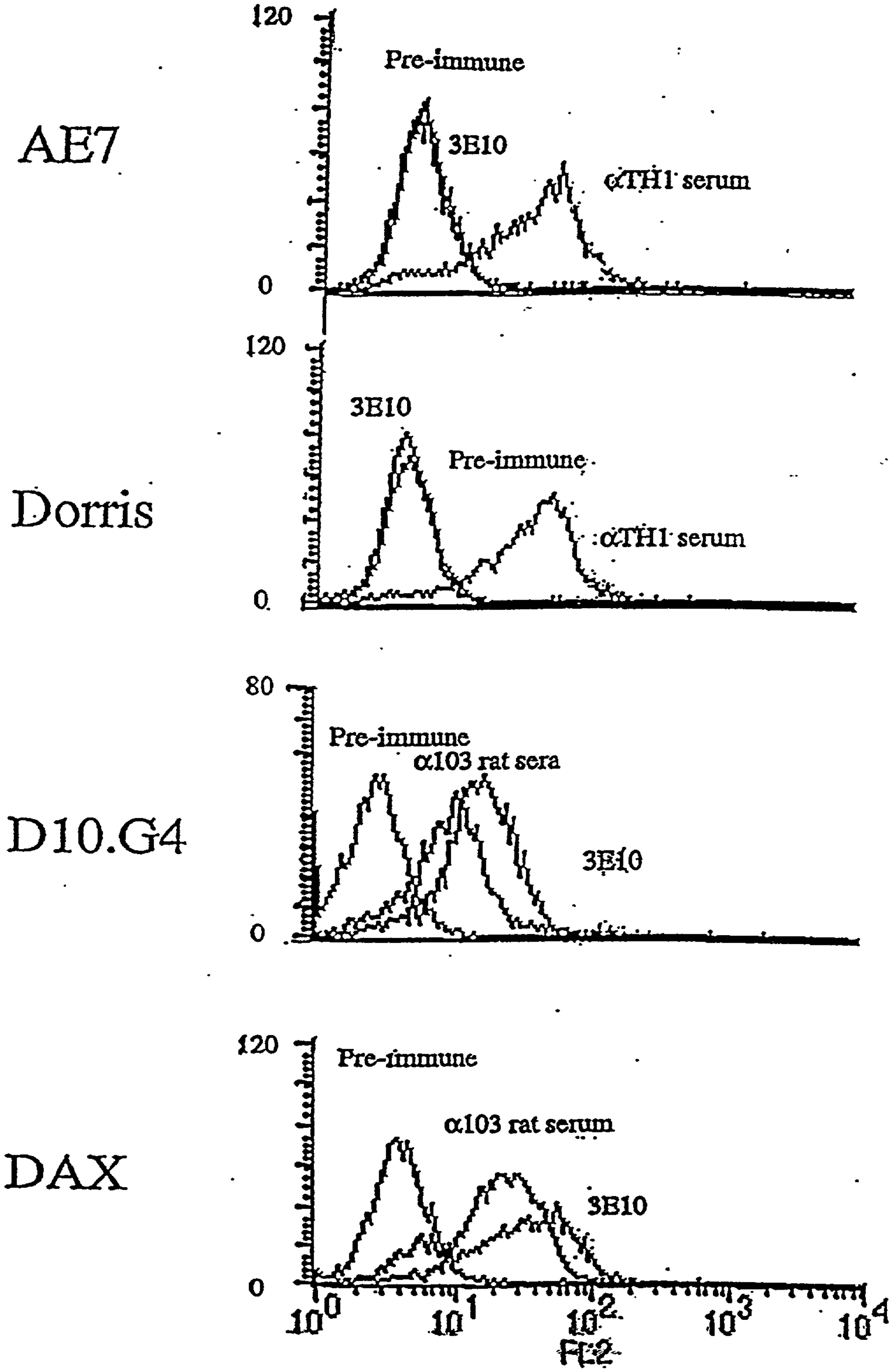
AE7
120
Pre-immune
3E10
αTH1 serum
0
Dorris
120
3E10
Pre-immune
αTH1 serum
0
D10.G4
80
Pre-immune
α103 rat sera
3E10
0
DAX
120
Pre-immune
α103 rat serum
3E10
0
10^0
10^1
10^2
10^3
10^4
FL2

FIGURE 25

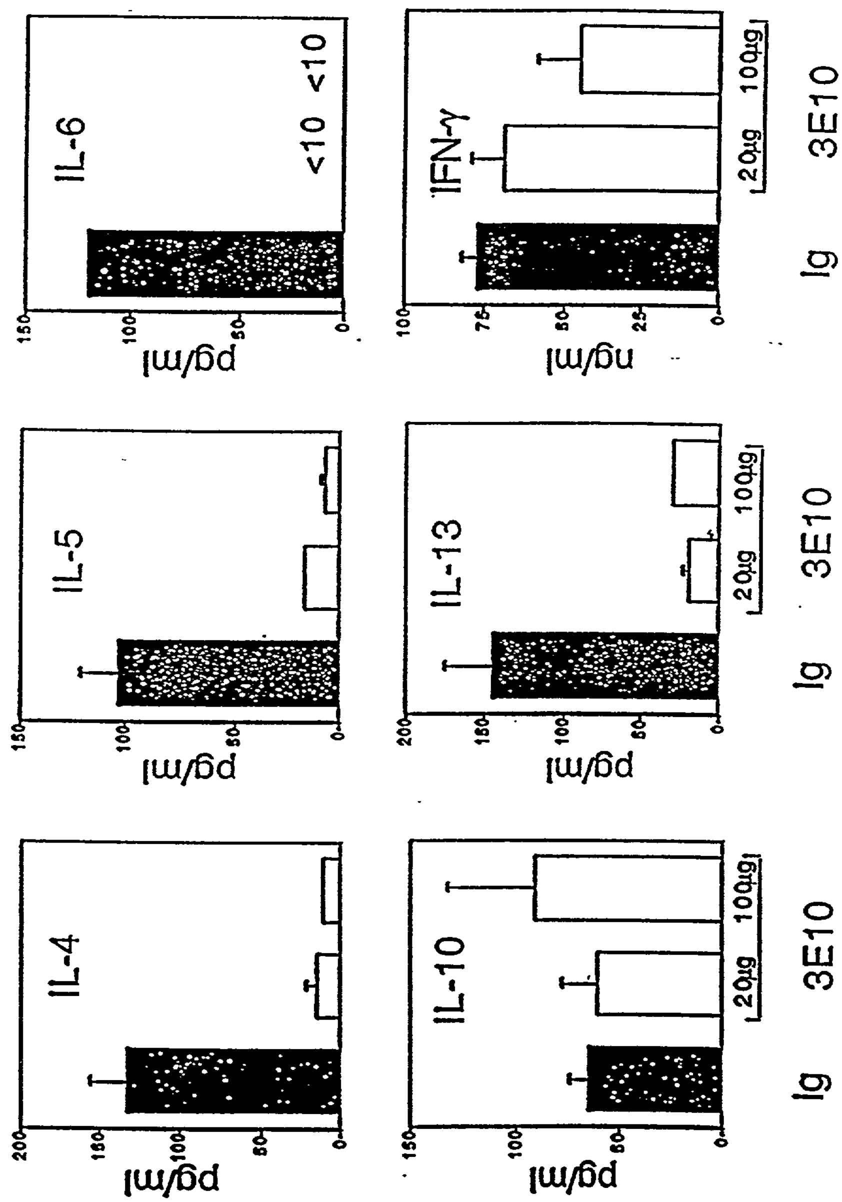

FIGURE 26

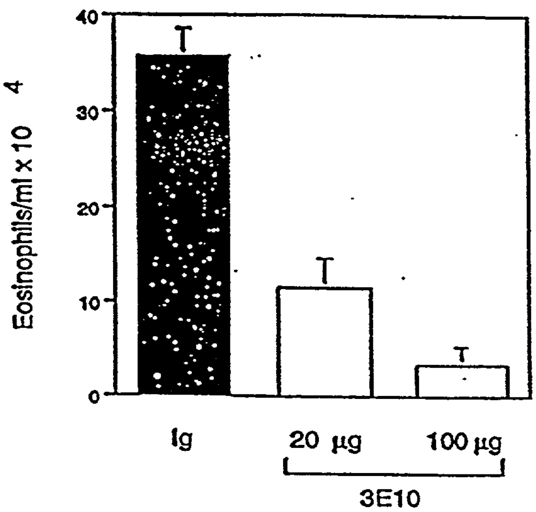

FIGURE 27 A

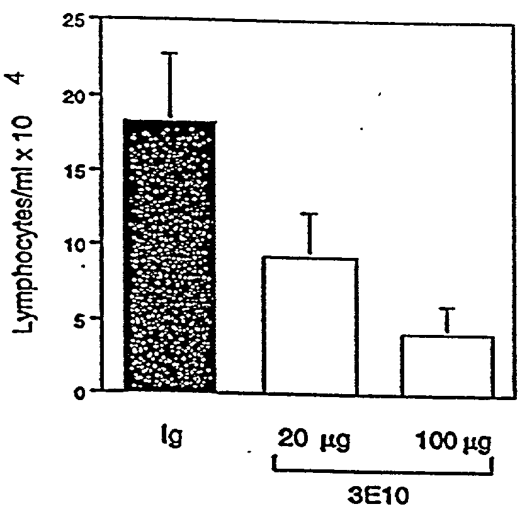

FIGURE 27 B

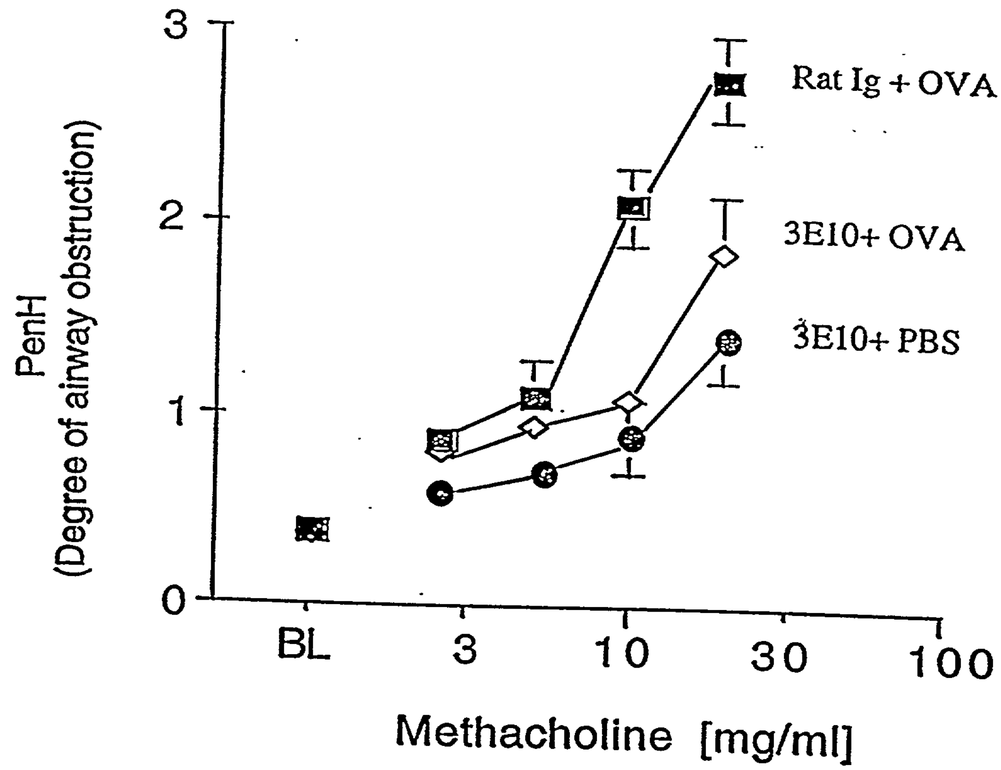
3
2
1
0
PenH
(Degree of airway obstruction)
Rat Ig + OVA
3E10+ OVA
3E10+ PBS
BL
3
10
30
100
Methacholine [mg/ml]

FIGURE 28

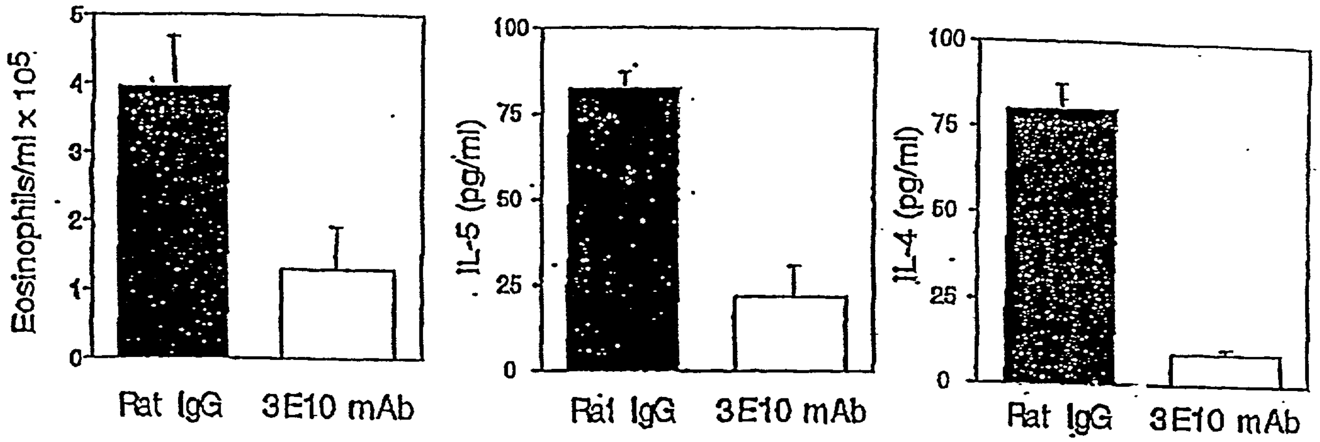

FIGURE 29A

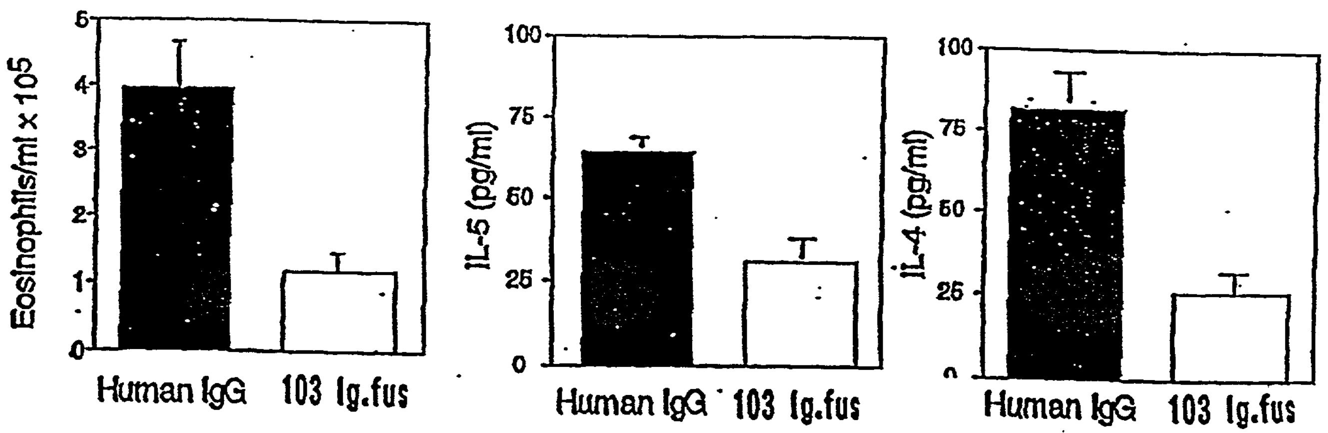

FIGURE 29B

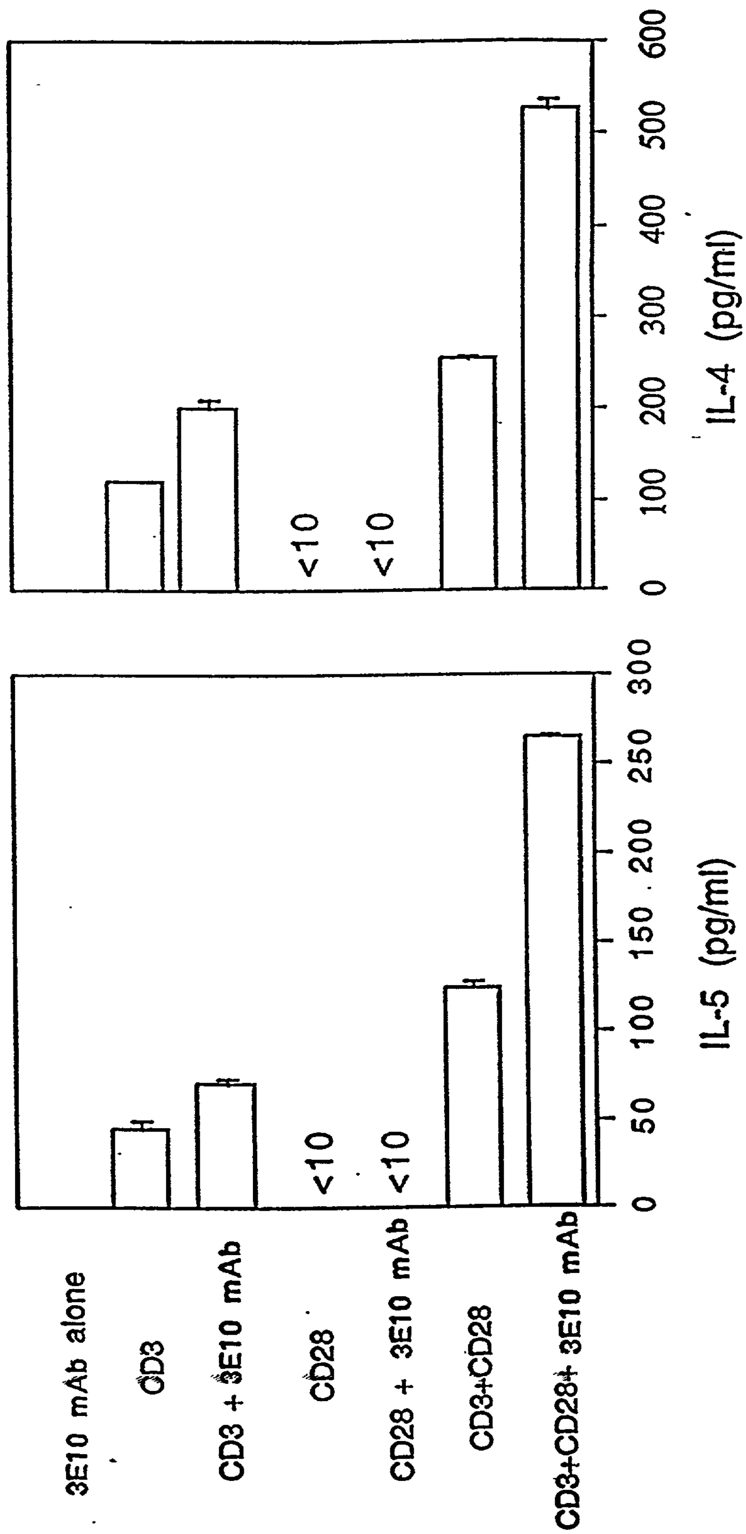
3E10 mAb alone
CD3
CD3 + 3E10 mAb
CD28
CD28 + 3E10 mAb
CD3+CD28
CD3+CD28+ 3E10 mAb
<10
<10
<10
<10
0
50
100
150
200
250
300
IL-5 (pg/ml)
0
100
200
300
400
500
600
IL-4 (pg/ml)

FIG. 30

Renal histology at 72hrs post reperfusion

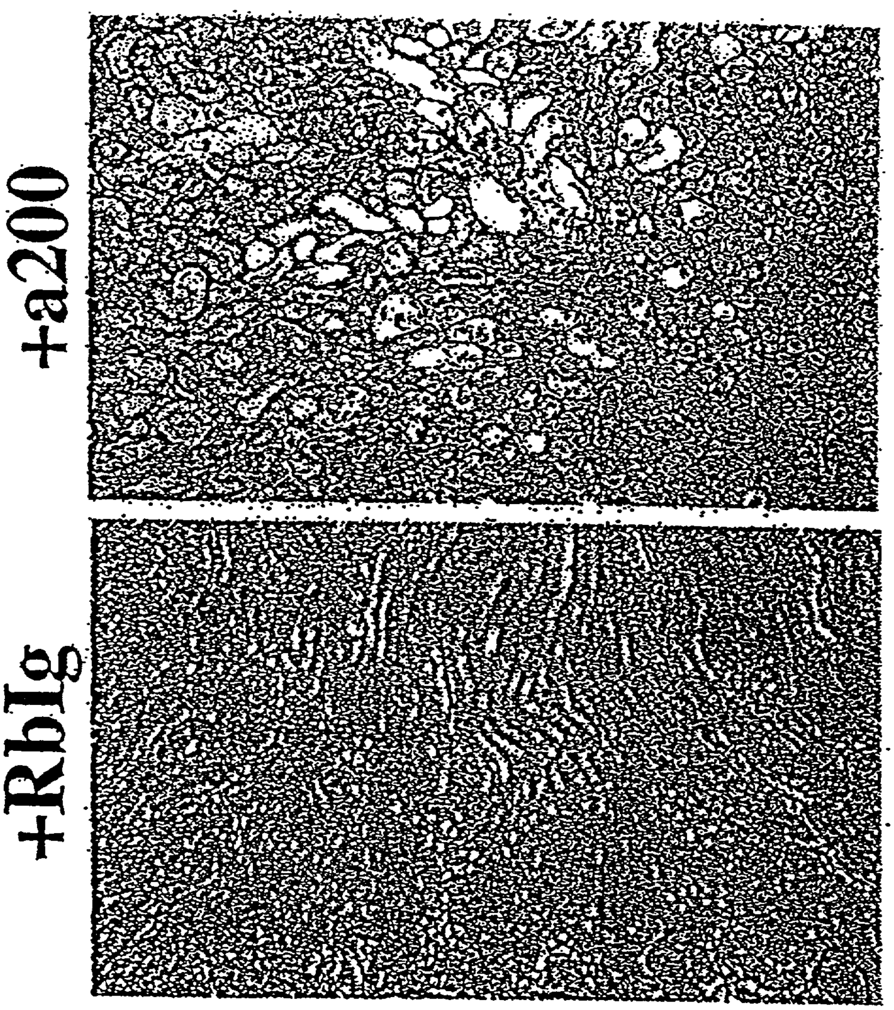

FIG. 31

Blockage of gene 200 during renal ischemia/reperfusion injury

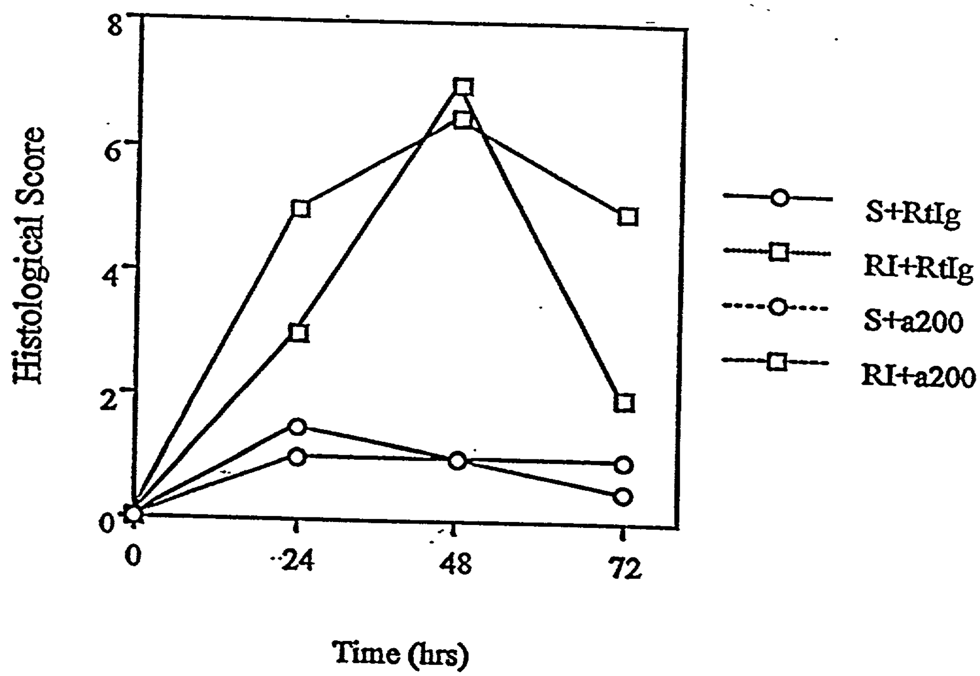

FIG. 32